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May 13, 2004, 16:19:57 ; Search time 47 Seconds (without alignments) 2012.955 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                               US-09-913-770B-1
1798
1 MNPFHASCWNTSAELLNKSW......QRRATEKEINNMGNTLKSHF 340
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCD7_NEW PUBL Pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCD7_NEW PUBL Pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUBL pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1145568 seqs, 278261457 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                                                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length DB	DB.	SUMMAKIES	Description
 	1798	100.0	340	10	US-09-791-932-117	Sequence 117, App
7	1798	100.0	340	10	US-09-990-940-2	Sequence 2, Appli
m	1798	100.0	340	10	US-09-964-923A-2	Sequence 2, Appli
4	1798	100.0	340	14	US-10-291-990-29	Sequence 29, Appl
S	1798	100.0	340	14	US-10-321-807-40	Sequence 40, Appl
9	1798	100.0	340	16	US-10-332-082-3	Sequence 3, Appli
7	1793	99.7	340	10	US-09-971-269-4	Sequence 4, Appli
ω	1792	99.7	340	14	US-10-225-567A-666	Sequence 666, App
6	1765	98.2	340	14	US-10-309-515-34	Sequence 34, Appl
10	1765	98.2	340	14	US-10-291-990-2	Sequence 2, Appli
11	1765	98.2	340	74	US-10-126-764-34	Sequence 34, Appl
12	1755	97.6	340	14	US-10-309-515-36	Sequence 36, Appl
13	1755	97.6	340	14	US-10-291-990-4	Sequence 4, Appli
14	1755	97.6	340	14	US-10-126-764-36	Sequence 36, Appl
15	1754.5	97.6	335	16	US-10-333-946-11	Sequence 11, Appl

equence 2 equence 2 equence 2 equence 2 equence 1 equence 1 equence 1 equence 2 equence 2 equence 2 equence 3 equence 3 equence 3 equence 3	Sequence 7, Appli Sequence 39, Appli Sequence 33, Appl Sequence 60, Appl Sequence 50, Appl Sequence 48, Appl Sequence 48, Appl Sequence 52, Appl Sequence 52, Appl Sequence 62, Appli Sequence 64, Appli Sequence 9, Appli Sequence 9, Appli
US. 10.2291.9 US. 10.2291.9	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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ALIGNMENTS

RESULT 1

110	7115-09-791-937-117	1-932-	117									
ś	Sequence	ce 117	Appli	Sequence 117, Application US/09791932	2760/SU	11932						
••	Publica	ation	No. US2	Publication No. US20030003451A1	451A1							
•••	GENERAL	L INFO	GENERAL INFORMATION:	 7								
••	APPLICANT:	CANT:	Vogeli	Vogeli, Gabriel	el							
••	APPLICANT:	CANT:	Parodi	Parodi, Luis A	Α.							
•-	APPLICANT	CANT:	Hiebsc	Hiebsch, Ronald	1d R.							
•-	APPLICANT		Lind,	Lind, Peter								
•-	APPLICANT		Kaytes	s, Paul	S							
	APPLICANT		Ruff,	Valerie								
••	APPLICANT		Huff,	Huff, Rita M.								
••	APPLICANT:		Wood,	Wood, Linda S.								
••	TITLE	OF IN	VENTION	No.	US2003	10003451A16	9] G	Protein	1-Couple	TITLE OF INVENTION: No. US20030003451Alel G Protein-Coupled Receptors Cross-Referer	Cross-R	Referen
•-	FILE 1	FILE REFERENCE:	NCE:	00325.US1	S1							
••	CURREI	AT APP	LICATIC	ON NUMBE.	R: US/C	CURRENT APPLICATION NUMBER: US/09/791,932						
. ••	CURRE	AT FIL	ING DAT	CURRENT FILING DATE: 2001-02-23	1-02-23							
•	PRIOR	APPLI	CATION	PRIOR APPLICATION NUMBER:	60/1	60/184,305						
••	PRIOR	FILIN	G DATE:	FILING DATE: 2000-02-23								
••	PRIOR		CATION	APPLICATION NUMBER:		60/184,304		,				
•	PRIOR		G DATE:	FILING DATE: 2000-02-23								
••	PRIOR		CATION	APPLICATION NUMBER: 60/184,303	60/1	.84,303						
•-	PRIOR		FILING DATE:		2000-02-23							
••	PRIOR		CATION	APPLICATION NUMBER: 60/184,397	60/1	.84,397						
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••	PRIOR		CATION	APPLICATION NUMBER:	60/1	60/184,247						
	PRIOR		G DATE:	FILING DATE: 2000-02-23	-02-23							
••	PRIOR		CATION	APPLICATION NUMBER:	60/1	60/188,880						
••	PRIOR		G DATE:	FILING DATE: 2000-03-13	-03-13	١.						
••	PRIOR		CATION	5		60/217,369						
••	PRIOR		FILING DATE:	2000								
••	PRIOR		CATION	APPLICATION NUMBER:		60/217,370						
٠.	PRIOR		FILING DATE:	2000	2000-07-11							
••	PRIOR		CATION	APPLICATION NUMBER:		60/218,492						
٠.	PRIOR	FILIN	FILING DATE:	2000	2000-07-20							
••	PRIOR	APPLI	CATION	APPLICATION NUMBER: 60/186,810	60/1	.86,810						
	PRIOR		G DATE:	FILING DATE: 2000-03-03	-03-03							
•	PRIOR	APPT,T	NOTTAN	APPLICATION NUMBER: 60/188.064	60/1	RR. 064						

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APPLICANT: PEDER, J. N.
APPLICANT: RAMANATHAN, C. S.
APPLICANT: RAMANATHAN, C. S.
APPLICANT: RAMANATHAN, C. S.
APPLICANT: RAMANATHAN, C. S.
APPLICANT: HAWKEN, D. R.
APPLICANT: CACACE, A.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY9,
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN AND TESTES
FILE REFERENCE: D0045NP
CURRENT FILING DATE: 2001-09-62
FRIOR APPLICATION NUMBER: 60/309,625
FRIOR FILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-01-16
FRIOR PLILING DATE: 2001-01-16
FRIOR PLILING DATE: 2000-09-27
FRIOR FILING DATE: 2000-09-27
FRIOR FILING DATE: 2000-09-27
FRIOR FILING DATE: 2000-09-27
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                                                                                                                                                                        OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR342, OTHER INFORMATION: melanin-concentrating hormone receptor 2 (MCHr2) US-09-990-940-2
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100.0%; Score 1798; DB 10; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.9e-167;
Matches 340; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                              Length 340;
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100.0%; Pred. No. 1.9e-167;
ive 0; Mismatches 0;
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                        SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 340
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Best Local Similarity 100.
Matches 340; Conservative
                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
  NUMBER OF SEQ ID NOS:
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US-09-964-923A-2
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LENGTH: 340
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APPLICANT: An, Songzhu
APPLICANT: Dai, Kangzhu
APPLICANT: Gupte, Jamila S.
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. US20030027252A1e1 Receptors
FILE REFERENCE: 018781-007410US
CURRENT FILING DATE: 2001-11-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1798; DB 10;
Pred. No. 1.9e-167;
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PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR PELLORION NUMBER: US 60/261,377
PRIOR APPLICATION NUMBER: US 60/279,554
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 60/186,457
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-06-23
PRIOR PELING DATE: 2000-06-23
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-07-14
NUMBER 09 SEQ ID NOS: 184
SOFTWARE: Patentin Version 3.0
SEQ ID NO 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09990940
Publication No. US20030027252A1
GENERAL INFORMATION:
APPLICANT: Tian, Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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Best Local Similarity 100.
Matches 340; Conservative
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Chen, Jin-Long
                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CONGANISM: Homo sapiens
US-09-791-932-117
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US-09-990-940-2
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APPLICANT: Chen. Rupong
APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G.
TITLE OF INVENTION: Receptors
FILE REFERENCE: ARRONGS
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US/10/714,008
PRIOR PELING DATE: 2000-11-16
PRIOR PELING DATE: 1990-11-17
PRIOR PELING DATE: 1990-12-23
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Pred. No. 1.9e-167;
Mismatches 0; Indels 0;
INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
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                                                                                                                                                     Sequence 40, Application US/10321807
Publication No. US20030166148A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%; Powatches 340; Conservative 0;
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ORGANISM: Homo sapiens
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Best Local Similarity 100.0%; Pred. No. 1.9e-167;
Matches 340; Conservative 0; Mismatches 0; Indels 0;
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; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-990-29
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                                                          STATEMENT: INFORMATION:

APPLICANT: SHIMOWURA, Yukio;
APPLICANT: SHIMOWURA, Yukio;
APPLICANT: Himowora, Yukio;
APPLICANT: HARDA, Mioko;
APPLICANT: HARDA, Mioko;
APPLICANT: HARDA, Mioko;
APPLICANT: SHINTANI, Yasushi
TITLE OF INVENTION: Method Screening MCH Receptor Antagonist/Agonist;
TITLE OF INVENTION: Method Screening MCH Receptor Antagonist/Agonist;
FILE REFERENCE: 2752 USOP
CURRENT FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: UF/1701/05809
PRIOR PILING DATE: 2001-07-05
PRIOR FILING DATE: 2001-07-05
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 3
LENGTH: 340
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; Beduence 4. Application US/09971269
; Publication No. US2030148281A1
; GENERAL INFORMATION:
    APPLICANT: Millennium Pharmaceuticals, Inc.
    APPLICANT: MILLE OF INVENTION: TRANSMEMBRANE RECEPTORS AND USES THEREOF
    FILE REPERENCE: MPTOO 414 PIRRM
    CURRENT APPLICATION NUMBER: US/09/971,269
    CURRENT APPLICATION NUMBER: US 60/237,700
    PRIOR APPLICANION NUMBER: US 60/237,700
    PRIOR PILING DATE: 2000-10-05
    NUMBER OF SEQ ID NOS: 20
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 4
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100.0%; Pred. No. 1.9e-167;
ive 0; Mismatches 0;
Sequence 3, Application US/10332082
Publication No. US20040086941A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 340; Conservative
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ORGANISM: Human
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Sequence 666, Application US/1022567A

Sequence 666, Application US/1022567A

Publication No. US20030113798A1

GENERAL INFORMATION

APPLICANT: LifeSpan Biosciences

APPLICANT: Brown, Joseph P.

APPLICANT: Brown, Christine L.

APPLICANT: Roush, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

FILE REPERENCE: 1920-4-4

CURRENT APPLICATION NUMBER: US/10/225,567A

CURRENT FILING DATE: 2001-12-19

FRIOR APPLICATION NUMBER: 60/257,144

PRIOR PELING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 2292

SOFTWARE: PatentIn version 3.1

SEQ ID NO 666

LINGTH: 340
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                                                                                                                        Length 340;
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99.7%; Score 1792; DB 14;
Best Local Similarity 99.7%; Pred. No. 7.3e-167;
Matches 339; Conservative 0; Mismatches 1;
                                                                                                                     ; Score 1793; DB 10;
; Pred. No. 5.8e-167;
. 0; Mismatches 1;
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (245)...(245)
CTHER INDEMATION: Unknown Amino Acid
US-10-225-567A-666
                                                                                                                        Query Match
Best Local Similarity 99.7%;
Matches 339; Conservative
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-269-4
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; ORGANISM: Macaca fascicularis
US-10-291-990-2
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 34
LENGTH: 340
TYPE: PRT
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TYPE: PRT
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SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
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| APPLICANT: Bennett Kinrade, Michele |
| APPLICANT: Brodbeck, Robbin M. |
| APPLICANT: Waters, Stephen M. |
| TITLE OF INVENTION: Melanin Concentrating Hormone Receptors |
| TITLE OF INVENTION: Moment In S/10/202. |
| CURRENT APPLICATION NUMBER: 00/284, 835 |
| PRIOR APPLICATION NUMBER: 00/284, 835 |
| PRIOR APPLICATION NUMBER: 10/126, 764 |
| PRIOR FILING DATE: 2002-04-18 |
| CRAWARE: Patentin version 3.1 |
| SEQ ID NO 34 |
| TYPE: PRI |
| TYPE: PRI |
| ORGANISM: Macaca fascicularis |
| US-10-309-515-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 34, Application US/10309515; Publication No. US20030114644A1; GENERAL INFORMATION:
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Sequence 2, Application US/10291990
Publication No. US20030148457A1
GENERAL INFORMATION;
APPLICANT: Bennett Kinrade, Michele
APPLICANT: Bennett Kinrade, Michele
APPLICANT: Bennett Kinrade, Michele
APPLICANT: Waters, Stephen
APPLICANT: Waters, Stephen
APPLICANT: Waters, Stephen
APPLICANT: Waters, James E.
TITLE OF INVENTION: Womes E.
TITLE OF INVENTION: Womes E.
TILE REFERENCE: NOI.2102
CURRENT APPLICATION NUMBER: US/10/291,990
CURRENT APPLICATION NUMBER: 60/350,493
FRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 2.
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| Publication No. US20030166834A1
| SENERAL INPORMATION:
| APPLICANT: Bennett Kinrade, Michele
| APPLICANT: Bennett Kinrade, Michele
| APPLICANT: Reause, James
| TITLE OF INVENTION: MELANIN CONCENTRATING HORMONE RECEPTORS
| FILE REFERENCE: NOO.2102
| CURRENT APPLICATION NUMBER: US/10/126,764
| CURRENT FILING DATE: 2002-04-18
| PRIOR APPLICATION NUMBER: 60/284,835
| PRIOR APPLICATION NUMBER: 60/284,835
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3; Mismatches
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ORGANISM: Macaca fascicularis
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US-10-291-990-4
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                                                                                                                            RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
                                                                                                                                                                 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
                                                                                                                                                                                     VESCAFDLISPDDVLWYILYITITFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
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                                                                1 MNPFHSSCWNTSAELSNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII
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                                              1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII
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APPLICANT: Beneat Kinrade, Michele
APPLICANT: Brodbeck, Robbin M.
APPLICANT: Brodbeck, Robbin M.
APPLICANT: Krause, James E.
TITLE OF INVENTION: Melanin Concentrating Hormone Receptors
FILE REFERENCE: NOO.2102C1
CURRENT APPLICANTON NUMBER: US/10/309,515
CURRENT APPLICANTON NUMBER: 60/284,835
PRIOR APPLICANTON NUMBER: 60/284,835
PRIOR APPLICANTON NUMBER: 10/126,764
PRIOR APPLICANTON NUMBER: 10/126,764
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
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                Indels
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Pred. No. 3.1e-163;
3; Mismatches 6;
 Pred. No. 3.2e-164;
3; Mismatches 5;
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11; Conservative 3
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ORGANISM: Macaca fascicularis
97.68;
 al Similarity 97.6
332, Conservative
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-10-309-515-36
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Best Local
Matches 33
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Sequence 4, Application US/10291990
; Sequence 4, Application US/10291990
; Publication No. US20030148457A1
; GENERAL INPORMATION:
   APPLICANT: Benett Kinrade, Michele
   APPLICANT: Brodbeck, Robbin M.
   APPLICANT: Waters, Stephen
   APPLICANT: Waters, Stephen
   TITLE OF INVENTION: Monkey and Canine Melanin Concentrating Hormone Receptors
   TITLE OF INVENTION NUMBER: US/10/291,990
   CURRENT FILING DATE: 2002-11-12
   PRIOR PELLING DATE: 2001-11-13
   NUMBER OF SEQ ID NOS: 34
   SOFTWARE: Patentin version 3.1
   SEQ ID NO 4
   LENGTH: 340
                                  61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
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US-10-126-764-36
Squence 36, Application US/10126764
Publication No. US20030166834A1
GENERAL INFORMATION:
APPLICANT: Bennett Kinrade, Michele
APPLICANT: Brodbeck, Robbin
APPLICANT: Brodbeck, James
TITLE OF INVENTION: MELANIN CONCENTRATING HORMONE RECEPTORS
FILLE REFERENCE: NOO. 2102
CURRENT APPLICALION NUMBER: US/10/126,764
CURRENT FILING DATE: 2002-04-18
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GENERAL INCOMPATION:
APPLICANT:
BURFORD, Nell; YUE.; LAL, Preeti G.
APPLICANT:
BURFORD, Nell; YUE.; Henry
APPLICANT:
GANDHI, Ameena R.; ELLIOTT, VICKI S.
APPLICANT:
RAMKUWAR, Jayalaxmi; BAUGHN, Mariah R.
APPLICANT:
RALLICK, Deborah A.; CHAMLA, Narinder K.
APPLICANT:
APPLICANT:
BURFORM:

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APPLICATION NUMBER: US 60/232,691
FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/284,835
PRIOR FILING DATE: 2001-04-19
NUMBER OF SEQ ID NGS: 58
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
LENGTH: 340
TYPE: PRT
TYPE: PRT
CREATER PRT
US-10-126-764-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/10333946
Publication No. US20040023252A1
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                                                                                                                                                                                                                       NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040023252A1 55002225CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
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Pred. No. 3.4e-163;
0; Mismatches 1; I)
PRIOR APPLICATION NUMBER: US 60/235,146
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 38
SCOTWARE: PERL Program
SEQ ID NO 11
LENGTH: 335
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Job time : 48 secs
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                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.2
Matches 334; Conservative
                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                              US-10-333-946-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                    Copyright
```

using sw model - protein search, OM protein

Run on:

May 13, 2004, 16:15:52; Search time 20 Seconds (without alignments) 1635.256 Million cell updates/sec

US-09-913-770B-1

1798 1 NNPFHASCWNTSAELLNKSWQRRATEKEINNMGNTLKSHF 340 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

length: 0 length: 2000000000

Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 st

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
	1 0	1				
4		TOO.	? ₹ ℃	7	7/67	g procein-coupled
7			422	N	C708	melanin-concentrat
m	468.5	•	363	7	I57940	somatostatin recep
4		25.4	418	7	4622	atin rec
ιΩ	4		391	7	179	
9	449	. 25.0	391	٥,	_	
7	4		391	(7)	929	tatin
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6	٥.		428	(7)	A44021	tatin
10	438.5		369	N	JC2083	
11	438	24.4	363	(A)	I57955	
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14			369	N	N	ü
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17	421.5		384	۲,	A47249	
18	418	23.5	388	(1	JN0605	in re
19	7		380	N	\vdash	н
20	17.		384	7	JC4629	ostatin
21	16.		380	0	482	opioido
22	080		380	~	4	opioid r
23	05.		380	0	55	opioid x
24	۳.		380	0	C23	opioid
25	ω 0		372	7	345	opioid
56	•		372	7	3853	ta opioid
27	σ		372	7	82	opioid
28	390		398	7	5651	mu opioid receptor
29	σ	21.7	398	7	75	oid rec

	mu opioid receptor	mu opiate receptor	opioid receptor mu	delta opioid recep	kappa opioid recep	opioid receptor ho	G protein-coupled	orphan opioid rece	G protein-coupled	G protein-coupled	thrombin receptor	angiotensin II rec	thyrotrophin-relea	thyroliberin recep	thyrotropin-releas	thyrotropin-releas
	56504	156553	865693	JE0087	149022	JC2421	56520	S43087	38973	38974	37912	JN0694	I56444	S23436	439251	N0708
,	T)	7	2	2 ن	. 2	2	2	2	2	2 I	2	2 ن	2 I	2	2	2 .
	398	400	392	373	367	367	367	370	328	333	425	362	411	412	393	398
,	51.6	21.6	21.5	21.2	20.0	20.0	20.0	19.8	19.7	19.0	18.3	18.2	17.7	17.7	17.4	17.3
	20	388	387	381.5	359.5	359.5	359.5	356.5	355	341.5	328.5	327.5	319	319	312.5	310.5
6	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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G protein-coupled receptor, SLT	receptor	- hum
C;Species: Homo sapiens (man)		

G protein-coupled receptor, SLT receptor - human C, Species: Howe sapiens (man)
C, Species: Howe sapiens (man)
C, Species: Howe sapiens (man)
C, Accession: UC7695
R, Mori M.; Harada, M.; Terao, Y.; Sugo, T.; Watanabe, T.; Shimomura, Y.; Abe, M.; Shint Biochem: Biophys. Res. Commun. 283, 1013-1018, 2001
A, Title: Cloning of a novel G protein-coupled receptor, SLT, a subtype of the melanin-oc A, Reference number: UC7695, MUD:21255282; PMID:11355873
A, Accession: UC7695
A, Contents: Hippocampus
A, Content

memory

C,Genetics: A,Gene: slt C;Superfamily: vertebrate rhodopsin C;Reywords: G protein-coupled receptor; transmembrane protein

Gaps ., Length 340; Indels Query Match
100.0%; Score 1798; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.5e-156;
Matches 340; Conservative 0; Mismatches 0;

9 9 1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 1 MNPFHASCWNTSAELLNKSWNKEFAYOTASVVDTVILPSMIGIICSTGLVGNILIVFTII à d

61 RSRKKTVPDIXICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120 61 ò d

240 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180 121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180 **VESCAFDLISPDDVLWYTLYLFITTFFFPLPLILVCYILLLCYTWEMYQQNKDARCCNPS** 181 121 ò 줨 δ 181 VESCAFDLISPDDVLMYTLYLTITTFFFPDPLILVCYILILCYTWEMYQQNKDARCCNPS 240 241 VPKORVMKLIKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300 엄 ਨੇ

241 VPKQRVMKLIKMYLVLVVVFILSAAPYHVIQLVNLQMCQPTLAFYVGYYLSICLSYASSS 300

g

301 INPFLYILLSGNFOKRLPQIQRRATEKEINNMGNTLKSHF 340 INPFLYILLSGNFOKRLPQIQRRATEKEINNMGNTLKSHF 340 301 à g

RESULT

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26.1%; Score 468.5;
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A,Cross-references: GDB:134187; OMIN:182453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSCANPLLYGFLSDNFRQSFRKV 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSSINPFLYILLSGNFOKRLPQI 320
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A,Introns: #status absent
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                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 35.3
Matches 114; Conservative
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A, Molecule type: DNA
A, Residues: 1-418 < COR>
C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: S32501
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NyAlternate names: somatotropin release-inhibiting factor subtype 28 receptor

NyAlternate names: somatotropin release-inhibiting factor subtype 28 receptor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 24-Nov-1999

C;Accession: IS7940; IS7940; Norman N.; Mahan, D.C.

Mol. Pharmacol. 42, 939-946, 1992

A;Reference number: IS7940; MUID: 93125499; PMID: 1362243

A;Reference number: IS7940; MUID: 93125499; PMID: 1362243

A;Reference number: IS7940; MUID: 9409238; PIDN: AAA17029.1; PID: 9409239

A;Reference number: IS7949; MUID: 94088493; PMID: 8264565

A;Cross-references: GB: Lodait, S.J.; Konig, M.; Mahan, D.C.

Mol. Pharmacol. 44, 1278, 1993

A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with prefix the molecular cloning and expression of a pituitary somatostatin receptor with prefix Scatus: preliminary; translated from GB/EMBL/DDBJ

A;Reference number: IS7949; MUID: 94088493; PMID: 8264565

A;Retus: preliminary; translated from GB/EMBL/DDBJ

A;Reterences: GB: S67370; NID: 94088493; PIDN: AAB29371.1; PID: 9455948

A;Cross-references: GB: S67370; NID: 940845947; PIDN: AAB29371.1; PID: 9455948

A;Cross-references: GB: S67370; MJ: Patel, Y.C.
Melanin-concentrating hormone receptor [validated] - human (SLC-1)
NyAlternate names: MCHR; orphan somatostatin-like receptor 1 (SLC-1)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: JC7080
R;Shimomura, Y:; Mori, M.; Sugo, T.; Ishibashi, Y.; Abe, M.; Kurokawa, T.; Onda, H.; Nis Blochem: Blophys: Res. Commun. 261, 622-626, 1999
A;Title: Isolation and identification of malanin-concentrating hormone as the endogenous A;Reference number: JC7080; MUD:99373129; PMID:10441476
A;Residues: 1-422 <SHI>
A;Residues: 1-422 <SHI>
A;Residues: 1-422 <SHI
A;Residues: 1-422 <SHI
A;Residues: 1-422 <SHI
A;Residues: 1-420 <SHI
A;Residues: 1-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLISPD-DVLWYTLYLIITTFFFP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 36.3%; Score 565.5; DB 2; Similarity 36.3%; Pred. No. 6.9e-44; 3; Conservative 61; Mismatches 114;
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398 AAQGQLRAVSN 408
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A;Accession: A46226
A;Molecule type: DNA
A;Cross-references: GB:M96738; NID:G338498; PIDN:AAA60592.1; PID:G338499
A;Cross-references: GB:M96738; NID:G338498; PIDN:AAA60592.1; PID:G338499
A;Note: sequence extracted from NCBI backbone (NCBIN:123685, NCBIP:123690)
A;Note: sequence extracted from NCBI backbone (NCBIN:123685, NCBIP:123690)
A;Cross-reference to Sequence extracted from NCBI backbone (NCBIN: G-)
A;Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays preference number: S32501; MUID:93238970; PMID:8097479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TM1>
F;44-70/Domain: transmembrane #status predicted <TM2>
F;91-106/Domain: transmembrane #status predicted <TM3>
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C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A46226; S32501
R;Yamada, Y; Reisine, T.; Law, S.F.; Ihara, Y.; Kubota, A.; Kagimoto, S.; Seino, M.; Se Not. Endocrinol. 6, 2135-2142, 1992
A;Title: Somatostatin receptors; an expanding gene family: cloning and functional charact A;Reference number: A46226; MUID:93149123; PMID:1337145
                                                                     somatosta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
submitted to the EMBL Data Library, August 1993
A;Description: Correction of the nucleotide and amino acid sequence of the rat
A;Reference number: S39244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 --NLSWPEPVGLWGAAFITYTSVLGFFGPLLVICLCYLLIVVKVKAAGMRVGSSR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 VPKORVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM----EQPTLAFYVGYYLSICLSYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 WIASAASSGNHNWS---LVGSASPMGARAVLVPVLYLLVCTVGLSGNTLV1YVVLRHAKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 TVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 AFDLISPDDV-LWYTLYLITIT---FFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS
                                                                                                                                          A;Accession: S39244
A;Molecule type: mRNA
A;Residues: 309-363 <PEN>
A;Cross-references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; PID:g433912
C;Genetics:
A;Gene: SSTR5
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 WNTSAELL-NKSWNKEFAYQTASVVD--TVILPSMIGIICSTGLVGNILIVFTIIRSRK-
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F;339/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                 cch 25.0%;
al Similarity 31.3%;
102; Conservative 6
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Best Local Similarity 31.3%
Matches 102; Conservative
                                                                 Query Match
Best Local Si
Matches 102,
                                                                                                                                                                                                                                                                           91
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F;159-181/Domain: transmembrane #status predicted <TW4>
F;203-233/Domain: transmembrane #status predicted <TW5>
F;255-282/Domain: transmembrane #status predicted <TW5>
F;255-282/Domain: transmembrane #status predicted <TW5>
F;289-316/Domain: transmembrane #status predicted <TW7>
F;17,30/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;116-191/Disulfide bonds: #status predicted
F;151,251,317,332/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
F;251/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
F;256/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted
F;212/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sometices -Homo sapiens (man)
C; Species -Homo sapiens (man)
C; Decies -Homo sapiens
R; Yamada, Y; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
R; Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
R; Manda, Mall, Acad. Sci. U.S.A, 89, 251-255, 1992
A; Title: Cloning and functional characterization of a family of human and mouse shades: 1.391 c.YaM.
A; Residues: 1.391 c.YaM.
A; Residues: 1.391 c.YaM.
A; Residues: 1.391 c.YaM.
A; Residues: 1.391 c.YaM.
A; Cross-references: GB: M81829; NID: G307433; PIDN: AAA58247.1; PID: G307434
A; Note: sequence extracted from NCBI backbone (NCBIN: 74767, NCBIP: 74768)
C; Genetics: sequence extracted from NCBI backbone (NCBIN: 74767, NCBIP: 74768)
A; Map position: 14q13-44q13
A; Cross-references: GDB: 134185; OMIN: 182451
A; Cross-references: GDB: 144185
A; Cross-references: GDB: 144186
A; Cross-references: GDB: 144186
A; Cross-references: GDB: 144186
A; Cr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VYSKVIKFKDGVESCAFDLISPDDVLW---YTLYLIITTFFFFLPLILVCYILILCYTWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYQQNKDARCCNPSVPKQR---VMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM----EQPT
                                                                                                                                                                                                                                                                                                                                                                                                1 MNPFHASCWNTSAELLNKS--WNKEFAYQTAS------VVDTVILPSMIGIICSTGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 TSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
                                                                                                                                                                                                                                                                                                 Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAFYVGYYLSICLSYASSSINPFLYILLSGNFOKRLPQIQRRATEK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                         25.4%; Score 456.5; DB 2; 32.4%; Pred. No. 6.2e-34; ive 75; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     somatostatin receptor 1 - human
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 32.4
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170
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C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Accession: C41795
R.Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A.?Title: Cloning and functional characterization of a family of human and mouse A.Reference number: A41795; MUID:92108031; PMID:1346068
A.Accession: C41795
C.Superfamily: vertebrate rhodopsin
C; Reywords: G protein-coupled receptor; hormone receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse
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                                                                                                                                                                                                                        ---HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTR 147
                                                                                                                                                                                                                                                                                                                                                                         257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---HOWARGGEWVEGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTR 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVAKVVNLGVWVLSLLVILPIVVFSRTAANSDGTVACNMIMPEPAQRWLVGFVLYTFLMG 231
                                                                                                                                              59 ILISFIYSVVCLVGLCGNSMVIYVILRYAKMKTATNIYILNLAIADELLMLSVPFLVTST
                                                                                                                                                                                                                                                           119 LLRH------WPFGALLCRLVLSVDAVNMFTSIYCLTVLSVDRYVAVVHPIKAARYRRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                206 FFFPLPLILVCYILILCYT-----WEMYQQNKDARCCNPSVPKQRVMKLTKMYLVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KITLMVMMVV
                                                                                                             35 VILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLI---
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// Score 449; DB 2; Length 39;
// Pred. No. 2.8e-33;
67; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 FLLPVGAICLCYVLIIAKWRMVALKAGWQ--QRKRSER-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 PQI----QRRATEKEINNMGNTLKS
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A; Reference number: S30508; MUID: 93066220; PMID: 1279674
                                                                                                                                                                                                           Best Local Similarity
Matches 108; Conserv
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S30508
S10508
Sprobable G protein-coupled receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: S30508
R;Meyerhof, W.; Wulfsen, I.; Schoenrock, C.; Fehr, S.; Richter, D.
Proc. Natl. Acad. Sci. U.S.A. 89, 10267-10271, 1992
A;Title: Molecular cloning of a somatostatin-28 receptor and comparison of its expression
                                                                                                                                                                                                                                                                                                 receptor expresse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane protein
                                                                                                                                                                                                                                                                                                                                                       A, Molecule type: mRNA
A, Residues: 1-391 <MEY>
A, Cross-references: GB:X62214; GB:X61630; NID:g56309; PIDN:CAA44193.1; PID:g56310
A, Cross-references: Drain
A, Dross-references: Drain
A, Note: It is uncertain whether Met-1 is the initiator or whether translation is i
R, Li, X.J.; Forte, M.; North, R.A.; Ross, C.A.; Snyder, S.H.
J. Biol. Chem. 267, 21307-21312, 1992
A, Title: Cloning and expression of a rat somatostatin receptor enriched in brain.
A, Reference number: A45102; MUID:93016064; PMID:1400442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90
                                                                                                                                                  somatostatin receptor - rat
N'Alternate names: probable G-protein-coupled receptor; SRIF receptor
C'species: Ratus norregiuse (Norway rat)
C'bate: 03-Aug-1992 #sequence-revision 03-Aug-1992 #text_change 24-Nov-1999
C'batesion: A39297; A45102; $20088
R',Meyerhof, W.; Paust, H.J.; Schoenrock, C.; Richter, D.
DNA Cell Biol. 10, 689-694, 1991 anovel putative G-protein-coupled receptoric Cloning of a cDNA encoding a novel putative G-protein-coupled receptoric number: A39297; MUID:92096119; PMID:1661599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 ILISPIYSVVCLVGLCGNSMVIYVILRYAKMKTATNIYILNLAIADELIMLSVPFLVTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---WEMYQQNKDARCCNPSVPKQRVMKLTKMVLVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLLPVGAICLCYVLIIAKWRMVALKAGWQ--QRKRSER------KITLMVMMVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---HOWARGGEWVFGGPLCTIITSLDTCNOFACSAIMTVMSVDRYFALVQPFRLTRWRTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 VILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:116692)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-391 <LII>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
25.0%; Score 449; DB 2; Length 39
Best Local Similarity 31.3%; Pred. No. 2.8e-33;
Matches 102; Conservative 67; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PQI-----QRRATEKEINNMGNTLKS 338
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                   POI
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R;Yasuda, K.; Rens-Domiano, S.; Breder, C.D.; Law, S.F.; Saper, C.B.; Reisine, T.; Be J. Biol. Chem. 267, 20422-20428, 1992
A;Title: Cloning of a novel somatostatin receptor, SSTR3, coupled to adenylylcyclase. A;Reference number: A44021; MUID:93018924; PMID:1328199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGVESCAFDLISPDDVLWYTLYLITT---FFFPLPLILVCYILILCYTWEMYQQNKDAR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCNPSVP-----KQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM----EQPTLAFYVG 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         somatostatin receptor SSTR3 - mouse
C,Species: Mus musculus (house mouse)
C,Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 PLDTTLGNTSAG------ASLTGLAVSGILISLVYLVVCVVGLLGNSLVIYVVLRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 SRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 ACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNPFHA-SCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTI
                                                                                                                                                                                                                                                                                                                                                14 IDPGNASSAMPLDTSLGNASAGTSLA---GLAVSGILISLVYLVVCVVGLLGNSLVIXVV
                                                                                                                                                                                                                                                                                                                                                                                                                   60 IR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDICNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 PFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTIIR-
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A;Cross-references: GB:M91000; NID:g201065; PIDN:AAA40144.1; PID:g201066
A;Cross-references: GB:M91000; NID:g201065; PIDN:AAA40144.1; PID:g201066
A;Note: sequence extracted from NCBI backbone (NCBIP:115746)
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
A, Accession: $30508
A) Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-428 <MEY.
A; Cross-references: EMBL: X63574; NID:g56315; PIDN:CAA45130.1; PID:g56316
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YYLSICLSYASSSINPFLYILLSGNFOKRLPQIORRATEK 327
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31.8%; Pred. No. 1.8e-32;
tive 71; Mismatches 130;
                                                                                                                                                                                                       24.6%; Score 441.5; DB 2;
llarity 31.8%; Pred. No. 1.5e-32;
Conservative 73; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 31.8
Matches 107; Conservative
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Bell,

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
R;Accession: 15,7955
Mol. Pharmacol. 45, 417-427, 1994
A;Reference number: 157955; MUID:94195267; PMID:7908405
A;Accession: 157955
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E;70-102/Domain: transmembrane #status predicted <TM2>
E;114-1135/Domain: transmembrane #status predicted <TM3>
E;115-177/Domain: transmembrane #status predicted <TM4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A-ASFWPFGPVLCRLVWTLDGVNQFTSVFCLTVMSVDRYLAVVHPLSSARWRRPRVAKLA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209
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214 LLVICLCYLLIVV---KVRAAGVRVGC----VRRRSERKVTRMVLVVVLVFAGCWLPFFT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     somatostatin receptor 5 - human
C;Species: Home sapiens (man)
C;Date: 30-Sep_1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 SAAAWVLSLCMSLPLLV----FADVQEGGTCNASWPEPVGLWGAVFIIYTAVLGFFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 VILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLGLWAASFILALPVWYSKVIKFKDGVESCAFDLTSPDDV-LW---YTLYLTITTFFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB:L14865; NID:g431094; PIDN:AAA20828.1; PID:g431095 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270 IQLVNLQMEQPTLAFYVG-YYLSICLSYASSSINPFLYILLSGNFQKRLPQI 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Score 438; DB 2; Length 36; Pred. No. 2.6e-32; 58; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: GDB:SST
A;Cross-references: GDB:119604, OMIM:182450
A;Map Dosition: 3928-3928
C;Superfamily: vertebrate rhodopsin
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A,Cross-references: GDB:138452; OMIW
A,Map position: 16p13.3-16p13.3
A,Introns: #status absent
C;Superfamily: vertebrate rhodopsin
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Best Local Similarity 35.6%;
Matches 104; Conservative 5
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A; Residues: 1-364 < YAM>
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F; 74-16; Domain: transmembrane #status predicted cTM2>
F; 117-138; Domain: transmembrane #status predicted cTM3>
F; 158-182; Domain: transmembrane #status predicted cTM3>
F; 158-218; Domain: transmembrane #status predicted cTM3>
F; 254-2286; Domain: transmembrane #status predicted cTM3>
F; 254-236; Domain: transmembrane #status predicted cTM3>
F; 256/Binding site: phosphate (Cys) (covalent) #status predicted
                                            249 VQAPACQRRRRSERRVTRWVVAVVALFVLCHWPFYLLNIVNVVCPLPEEP--AFPGLYFL 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SERVITINIXILINIAIADELFMLGLPFLAMQVAL-VHWPFGKAICRVVMTVDGINQFTS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VESCAFDLISPDDVLWYT---LYLTITTFFFDLDLILVCYILILCYTWEMYQQNKDARCC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPFDL---NGSVATANSSNQTEPYYDLTS---NAVLTFIYFVVCIIGLCGNTLVIYVILR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                somatostatin receptor 2 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Acession: JG2083
R;Matsumoto, K.; Yokogoshi, Y.; Fujinaka, Y.; Zhang, C.; Saito, S.
Biochem: Biophys. Res. Commun. 199, 298-305, 1994
A;Title: Molecular cloning and sequencing of porcine somatostatin receptor 2
A;Reference number: JG2083; MUID:94168590; PMID:8123027
ESCAFDLTSPDDVLWYT - - - LYLTITTFFFPLFLILVCYILILCYTWEMYQQNKDARCCN
                                                                                                                                                        ---KORVMKLTKMVLVLVVVFILSAAPYHVIQLVNLOM----EQPTLAFYVGYYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:D21338; NID:g415606; PIDN:BAA04810.1; PID:g472306 C;Comment: This protein inhibits growth hormone release. C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 369;
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                                                                                                                                                                                                                                                                                                    SICLSYASSSINPFLYILLSGNFOKRLPQIORRATEK 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASSSINPFLYILLSGNFOKRLPQI 320
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Best Local Simi
Matches 103;
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somatostatin receptor, somatotropin release-inhibiting factor receptor, SRIF receptor
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                                                                                                                                                          Somatostatin receptor 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-58p-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999
C;Accession: D41795; IS6236
C;Accession: D41795; IS6236
R;Yamada, Y; Post, S:R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 VVDTVILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 LVPLTIICLCYLFII-----IKVKSSGIRVGSŠKRKKSEKKVTRMVSIVVAVFIPCWLP
                 DIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMS
                                                                                                                        129 UDRYFALVOPFRLIRWRIRXKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDL
                                                                                                                                                                                                                                                                                                                                          246 VMKLIKMVLVLVVVFILSAAPYHVIQLVNLQME-QPTLAFYVGYYLSICLSYASSSINPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 MISNAVLTFIYFVVCVVGLCGNTLVIYVLLRYAKMKTITNIYILNLALADELFMLGLPFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 TIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDDVLWYT---LYLTITTF
                                                                                                                                                                                                                                                                                      PG-BSGAWYTGFIIYTFILGFLVPLTIICLCYLFII-----IKVKSSGIRVGSSKRKKS
                                                            189 ISPDDVLWYT---LYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Residues: 1.369 «KIU»
A.Cross-references: GB:M3373; NID:g207026; PIDN:AAA42165.1; PID:g207027
A.Cross-references: GB:M3373; NID:g207026; PIDN:AAA42165.1; PID:g207027
A.Note: sequence extracted from NCBI backbone (NCBIN:102315, NCBIP:102316)
C.Superfamily: vertebrate rhoopsin
C.Superfamily: vertebrate rhoopsin
C.Keywords: G protein-coupled receptor; transmembrane protein
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R;Kluxen, F.W.; Bruns, C.; Lubbert, H.
Proc. Natl.: Acad. Sci. U.S.A. 89, 4618-4622, 1992
A;Title: Expression cloning of a rat brain somatostatin receptor CDNA.
A;Reference number: A45291; WUID:92262491; PMID:1374909
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ses 94; Conserv
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A; Status: preliminary
A; Molecule type: mRNA
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Best Local Si
Matches 94,
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C,Species: Homo sapiens (man)

C,Date: 31-be-1993 #sequence_revision 31-be-1993 #text_charge 24-Nov-1999

C,Accession: B41795

R,Yamada, Y, Poet, S.R., Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.

Proc. Natl. Acad. Sci. US.A. 89, 251-255, 1992

A;Title: Cloning and functional characterization of a family of human and mouse somatost

A;Reference number: A41795; MUID:92108031; PMID:1346068

A;Rocession: B41795

B41717138/Domain: transmembrane #status predicted < TM5>
A;Rocession: B41705

B41717138/Domain: transmembrane #status predicted < TM5>
A;Rocession: B41705

B41717138/Domain: transmembrane #status predicted < TM5>
A;Rocession: B4170
F;280-307/Domain: transmembrane #status predicted <TM7>
F;13,26,187/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;112-186/Disulfide bonds: #status predicted
F;242,325/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pr
F;247/Binding site: phosphate (Thir) (covalent) (by cAMP-dependent kinase) #status predic
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#status predicted
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LLVICLCYLLIVV---KVRAAGVRVG----VRRRSBRKVTRMYLVVVLVFAGCWLPFFT 266
                                                                                                                                                                                                                                                                                                                                       ARGGEWVFGGPLCTIITSLDTCNOFACSAIMTVMSVDRYFALVOPFRLTRWRTRYKTIRI 153
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                                                                                                                                                                                                                                                                                                       VILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHQW
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                                                                                                                                                                                             24.4%; Score 438; DB 2; Length 364 clarity 35.6%; Pred. No. 2.6e-32; Conservative 58; Mismatches 110; Indels.
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Best Local S:
Matches 101,
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Best Local S:
Matches 104
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Gaps

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A)Residues: 1-369 <PAM>
A)Cross-references: GB:M81832; NID:g201060; PIDN:AAA58256.1; PID:g201061

A)Cross-references: GB:M81832; NID:g201060; PIDN:AAA58256.1; PID:g201061

B)Cross-references: GB:M81832; NID:g201060; PIDN:AAA58256.1; PID:g201061

A)CRETING TO THE TOWN THE T
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Ittle: Cloning and functional characterization of a family of human and mouse somatost
A;Reference number: A41795, MUID:92108031, PMID:1346068
A;Accession: D41795
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A;Nolecule type: mRNA
A;Residues: 99-309 <RES.
A;Residues: 99-309 <RES.
A;Cross-references: GB:S71756; NID:g560631
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein
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                                                                                                                                                                                                                                      A;Status: nucleic acid sequence not shown A;Molecule type: DNA
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Search completed: May 13, 2004, 16:20:27 Job time : 21 secs

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May 13, 2004, 16:09:06; Search time 18 Seconds (without alignments) 983.547 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-913-770B-1 1798 I MNFFHASCWNTSAELLNKSW......QRRATEKEINNMGNTLKSHF 340 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

141681

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_42:* Database :

SUMMARIES

	Description	Q969v1 homo sapien	macaca	Q8sq54 macaca fasc	rattus	mus mus	Q8mj89 macaca mula	Q99705 homo sapien		O08858 mus musculu	homod		mus n	P28646 rattus norv					P35346 homo sapien		mus m	P30680 rattus norv				P49660 mus musculu		cavie	рошоц	homod	P33533 rattus norv	P32300 mus musculu	sns /	soq
	ID	MCR2 HUMAN	MCR2 MACMU	MCR2 MACFA	MCR1 RAT	MCR1 MOUSE	MCR1 MACMU	MCR1 HUMAN	SSR5 RAT	SSR5_MOUSE	SSR3 HUMAN	SSR1 HUMAN	SSR1_MOUSE	SSR1 RAT	SSR2 BOVIN	SSR3_RAT	SSR3_MOUSE	SSR2_PIG	SSR5_HUMAN	SSR2_HUMAN	SSR2_MOUSE			SSR4_HUMAN		SSR4_MOUSE	OPRK_MOUSE	OPRK_CAVPO	OPRK_HUMAN	OPRD HUMAN	OPRD_RAT	OPRD MOUSE	OPRM PIG	OPRM_BOVIN
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ALIGNMENTS

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VESCAFDLTSPDDVLWYTLYLTTTFFFPLPLTLLVCYTWEMYQQNKDARCCNPS
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                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                            -:- FUNCTION: Receptor for melanin-concentrating hormone, coupled to proteins that activate phosphoinositide hydrolysis.
-:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- TISSUE SPECIFICITY: Specifically expressed in the brain, with highest levels in creebral cortex, hippocampus and amygdala. No expression detected in the cerebellum, thalamus or hypothalamus.
-:- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                             "Molecular characterization of a novel melanin-concentrating hormone receptor: evidence of its expression in lateral hypothalamus."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
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EXTRACELLULAR (POTENTIAL).

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7 (TOTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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R InterPro; IPR008362; MCH2_receptor.
InterPro; IPR008362; MCH2_receptor.
R InterPro; IPR008361; MCH_receptor.
R Pfau; Pr00001; 7tm 1; 1.
R PRINTS; PR001784; MCH2RCEPTOR.
R PRINTS; PR01783; MCH2RCEPTOR.
R PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
R PROSITE; PS00207; G PROTEIN RECEP_F1_2; 1.
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3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EMBL, AK029596; AAK38157.1; -.
EMBL, AR399937; AAL05528.1; -.
EMBL, AR390937; BAR32193.1; -.
EMBL, AB058849; BAB87842.1; -.
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Genew; HGNC:20867; GPR145.
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                                                                                                                                              241 VPKQRVMKLTKYVLVLVLVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
VPKQRVMKLTKMVLVLVVVPILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS

specific gene expression.",
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for melanin-concentrating hormone, coupled to proteins that activate phosphoinositide hydrolysis.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUB SPECIFICITY: Specifically expressed in the brain with highest levels in cerebral cortex, hippocampus and hypothalamus, and lower levels in caudate nucleus, putamen and thalamus.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tan C.P., Sano H., Iwaasa H., Pan J., Sailer A., Hreniuk D.L., Feighner S.D., Palyha O.C., Figueroa D.J., Austin C.P., Jiang M.M., Yu H., Ito J., Ito M., Ito M., Guan X.M., Kanatani A., Van der Ploeg L.H.T., Howard A.D.; "Melanin-concentrating hormone receptor subtypes 1 and 2: species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       none receptor 2 (MCH receptor 2) (MCHR-2) (MCH2) (G protein coupled receptor 145).
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 INPFLYILLSGNFOKRLPOIORRATEKEINNMGNTLKSHF 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
hormone receptor 2 (MCH
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InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR008362; MCH2_receptor.
InterPro; IPR008361; MCH_receptor.
Pfam; PP00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MCH-R2) (MCH2R) (MCH-2R) (MCH2)
GPR145 OR MCHR2.
Macaca mulatta (Rhesus macaque)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Puruichi K.;
"Molecular characterization of a novel melanin-concentrating hormone receptor: evidence of its expression in lateral hypothalamus.";
Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
-!-FUNCTION: Receptor for melanin-concentrating hormone, coupled to G proteins that activate phosphoinositide hydrolysis.
-!-SUBCELLULAR LOCATION: Integral membrane protein.
-!-SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Melanin-concentrating hormone receptor 2 (MCH receptor 2) (MCHR-2) (MCH-R2) (MCH-R2) (MCH-R2) (MCH-R2)
2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

4 (POTENTIAL).

EXTRACELULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

7 (POTENTIAL).

1 (POTENTIAL).
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Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Cercopithecinae; Primates; Catarrhini; Cercopithecidae;
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Pred. No. 4.5e-117;
Mismatches 5; Indels
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Kamohara M., Saito T., Soga T., Saito Y., Oda T., Masuho Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INPFLYILLSGNFOKRLPQIORRATEKEINNMGNTLKSHF 340
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97.1%;
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                       DB 1; Length 340;
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2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).

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Pred, No. 7.2e-117;
4; Mismatches 6;
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340 AA;
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Matches 330; Conserv
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MCRI RAT
ID MCRI RAT
AC P97639;
DT 01-NOV-1997 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20032718; PubMed=10559938; Lembo P.M.C., Grazzini E., Gao J., Hubatsch D.A., Pelletier M., Lembo P.M.C., St-Onge S., Pou C., Labrecque J., Groblewski T., O'Donnell D., Payza K., Ahmad S., Walker P.; "The receptor for the orexigenic peptide melanin-concentrating hormone is a G-protein-coupled receptor."; Mar. Cell Biol. 1:267-271(1999).
                                                                                                                                             Eukaryota, Mětazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 150-307 FROM N.A.
MEDLINE=97131607; PubMed=8977118;
Kolakowski L.F. Jr., Jung P.P., Nguyen T., Johnson M.P., Lynch K.R.,
Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.;
"Characterization of a human gene related to genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: Receptor for melanin-concentrating hormone, coupled to g proteins that inhibit adenyly1 cyclase.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- TISSUE SPECIFICITY: High level in the brain, moderate amounts in the eye and skeletal muscle, and small amounts in tongue and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99347736; PubMed=10421368; Saito Y., Nothacker H.P., Wang Z., Lin S.H., Leslie F., Civelli O.; "Molecular characterization of the melanin-concentrating-hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pituitary.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                   MEDLINE-98193144, PubMed-9531978,
Lakaye B., Minet A., Zorzi W., Grisar T.;
"Cloning of the rat brain cDNA encoding for the SLC-1 G protein-
coupled receptor reveals the presence of an intron in the gene.";
Biochim. Biophys. Acta 1401:216-220(1998).
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Melanin-concentrating hormone receptor 1 (MCH receptor 1) (MCHR-(MCH-11) (MCH-11) (MCH-11) (MCH-11) (MCH-11) (Gprotein coupled receptor 24) (Somatostatin receptor-like protein) (SLC-1) (Fragment).
GPR24 OR MCHR1 OR SLC1.
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InterPro; IPR0040276; GPCR Rhodesn.
InterPro; IPR004047; MCHL receptor.
InterPro; IPR004047; MCHL receptor.
InterPro; IPR004017; Ttm 1; 1.—
Pfam; PR00001; 7tm 1; 1.—
PRINTS; PR00207; MCHRECEPPOR.
PRINTS; PR010783; MCHRECEPPOR.
PRINTS; PR01783; MCHRECEPPOR.
PROSITE; PS00237; GPROTEIN RECEP F1 1; PALSE NEG.
PROSITE; PS00227; GPROTEIN RECEP F1 2; 1.
G-prorein coupled receptor; Transmembrane; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 398:253-258(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 400:265-269(1999)
                                                                                                                              Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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48 IIMPSVFGTICLLGIVGNSTVIFAVVKKSKLHWCSNVPDIFIINLSVVDLLFLLGMPFMI 107
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                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Melanin-concentrating hormone receptor 1. (MCH receptor 1) (MCHR-1)
(MCH-R1) (MCHR) (MCHR) (G protein coupled receptor 24)
(Somatostatin receptor-like protein) (SLC-1).
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                                                                                                                                                                                            N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lakaye B., Adamantidis A., Coumans B., Zorzi W., Parmentier M.,
Grisar T.,
                                                                                                                                                                                                                                                                           31.7%; Score 569.5; DB 1; Length 360;
                                                                                                                                                                                                                                                                                                           60; Mismatches 114; Indels
              2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                    -LINKED (GLCNAC. . .) (PC
B68D3C993E491350 CRC64;
                                                                            4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                       (POTENTIAL)
                                                                                                                                                                   7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423 AA.
                                                                                                                                       6 (POTENTIAL)
                                                                                                         (POTENTIAL)
                                                                                                                       CYTOPLASMIC
                                                                                                                                                                                                                                                                                              Pred. No. 2.
                                                                                                                                                                                                                                               39727 MW;
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                                                                                                                                                                                                                                                                                          36.78;
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                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      336 AAQGQLRTVSN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 ATEKEINNMGN 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-ILS, and ISS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Mouse)
                                                                                                                                                                                                                                            360 AA;
                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBL TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129/SvJ
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                                                                                                                                                                                                                                                                                                         Matches 114;
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TRANSMEM
                                                             DOMAIN
TRANSMEM
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TRANSMEM
                  RANSMEM
                                                                                                         RANSMEM
                                                                                                                                     TRANSMEM
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                                                                                            DOMAIN
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A Mikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Mikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Raldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Golobori T., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Ralda D., Brusic V., Chothia C., Corbani L.E., Cousins S., Ralda E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gariboldi M., Gissi C., Godzik A., Gough J., Ramana A., Kawaji H., Kawaswa Y., Kedrierski R., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Oi D., Ramachandran S., Ravasi T., Reed J.C., Reed J.J., Ring B.L., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Angashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Oi D., Ramachandran S., Ravasi T., Reed J.C., Reed J.J., Ring B.C., Ringala K., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Yang L., Yang L., Yang C., Wang C., Wang C., Wang T., Yang L., Yang L., Yang C., Wang C., Wang Y., Watanabe T., Konno H., Nakamura M., Sakazume N., Sakai K., Sakai K., Sasaki D., Shinagawa A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I., Hara A., Hashizume W., Imocani K., Ishii Y., Ichinagawa A., Harney E., Hayashizaki Y.; Sasaki D., Shinagawa R., Shinagawa A., Sakai K., Sasaki D., Shinagawa R., Shinagawa A., Satunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., R. Hayashizaki Y.; Waterston R., Lander E.S., Rogers J., R. Hayashizaki Y.; Waterston R., Lander E.S., Rogers J., R. Hayashizaki Y.; Sasaki D., Shinagawa G., Chinai P., Shinagawa A., Shinayasi Z., Sasaki D., Shinagawa C., Ishinayasaki A., Sasaki D., Shinagawa G., Chinai P., Shinagawa C., Shinagawa C., Shinagawa C., Shinagawa C., Shinagawa C., Shinagawa C., Shinay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Receptor for melanin-concentrating hormone, coupled to both 6 proteins that inhibit adenylyl cyclase and G proteins that activate phosphoinositide hydrolysis.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-!- CAUTION: It is uncertain whether Met-1 or Met-71 is the initiator.
MEDLINE=21363810; PubMed=11471062;
bringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
"High-throughput sequence identification of gene coding variants
                                                                                                                                                                                                        STRAIN=ILS, and ISS;
Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY276741; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished observations (JUL-2002).
                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-129 FROM N.A.
MEDLINE=22354683; PubMed=12466851;
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InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR004047; MCHI_receptor.
InterPro; IPR008361; MCH_receptor.
Pfam; PP00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONCEPTUAL TRANSLATION OF 1-129.
                                                                                                           within alcohol-related QTLs.";
Mamm. Genome 12:657-663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF498247; AAM22964.1; -.
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PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                 SEQUENCE OF 71-423 FROM N.A.
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171 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSMA 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 WAPYYVLQLIQESISRPILIFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP-----KQRVMKLTKMVLVLVVVFILS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 FVVITAAYVKIL------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 AAPYHVIQIVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFOKRLPQIQRR 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Melanin-concentrating hormone receptor 1 (MCH receptor 1) (MCHR-1)
(MCH-R1) (MCH-IR) (MCH-IR) (MCH-IR) (G protein coupled receptor 24)
                                                                                          CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCKAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Tan C.P., Sano H., Iwaasa H., Pan J., Sailer A., Hreniuk D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                              31.7%; Score 569.5; DB 1; Length 423; 36.7%; Pred. No. 3.2e-33; ive 60; Mismatches 114; Indels 23
PRINTS; PRO1507; MCHIRECEPTOR.
PRINTS; PRO1783; MCHRECEPTOR.
PROSITE; PRO0227; G PROTEIN RECEP F1 1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_PICCHEIN coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 114 EXTRACELLULAR (POTENTIAL).
TRANSMEM 115 137 1 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                 46269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecinae, Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 114; Conserv
                                                                                                                                                                                                                                                                                                                                                                               423 AA;
                                                                                                                                                                               2230
233
233
323
346
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Q8MJ89;
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210 LPLILVCYILII.CYTWEMYQQNKDARCCNPSVP-----KQRVMKLIKMVLVLVVVFILS
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                                                      256 FVVITAAYVRIL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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MCR1_HUMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
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                                                                                                                                                Fried S., O'Neill K., Hawes B.E.;

Fried S., O'Neill K., Hawes B.E.;

"Cloning and characterization of thesus monkey MCH-R1 and MCH-R2.";

"Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Receptor for melanin-concentrating hormone, coupled to both G proteins that inhibit adenylyl cyclase and G proteins that activate phosphoinositide hydrollysis (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Feighner S.D., Palyha O.C., Figueroa D.J., Austin C.P., Jiang M.M. Yu H., Ito J., Ito M., Ito M., Guan X.M., Kanatani A.,
                        Yu H., Ito J., Ito M., Ito M., Guan X.M., Kanatani A., Van der Ploeg L.H.T., Howard A.D.; "Melanin-concentrating hormone receptor subtypes 1 and 2: species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).

N.LINKED (GLORAC. .) (POTENTIAL).

N.LINKED (GLORAC. .) (POTENTIAL).

N.LINKED (GLORAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pfam; PF00001; 7tm i; 1.
PRIMES, PR0023; GPCRRHDODSN.
PRIMES; PR01783; MCHIRECEPTOR.
PRINTS; PR01783; MCHRECEPTOR.
PROSTIE; PS00237; G PROTEIN RECEP FL_1; FALSE_NEG.
PROSTIE; PS00237; G PROTEIN RECEP FL_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                       specific gene expression.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR000476; GPCR Rhodpsn.
InterPro; IPR004047; MCH_receptor.
InterPro; IPR008361; MCH_receptor.
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113; Conservative
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388 AA;
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Develocing From M. S. Mink E. S. Beare D.M., Burbham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M., Dunham I., Hunt A.R., Collins J.E., Barbskiewich R., Babbage A.K., Barguley C., Bailey J. Barlow K.F., Bates K.N., Beasley O.P., Barguley C., Bailey J. Barlow K.F., Bates K.N., Beasley O.P., Bardey S.E., Bridgeman A.M., Buck D., Burgess J., Burton J., Carder C., Carter N.P., Chen Y., Clark G., Collier R.E., Comor R., Conroy D., Cockree C., Dodsworth S.J., Durbin R.M., Blington A.G., Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Blington A.G., Brans K.L., Fey J.M., Fleming K., French L., Garner A.A., Blington A.G., G., L., Fey J.M., Fleming K., French L., Garner A.A., Glibert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C., All R. Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S., Martyn I.D., Mashredhi-Mohammadi M., Matthews L.H., Mccann O.T., Martyn I.D., Mashredhi-Mohammadi M., Minhe S.A., Mohuriay A.A., Milne S.A., Mohuriay A.A., Milne S.A., Mohuriay A.A., Milne S.A., Mohulimore B.J., C.T., Ohlings S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
                                                                                                                                                  ----ORMISSVAPASORSIRLRIKRVIRTAIAICLVFFVC 303
                                                                                                264 AAPYHVIQLWNLQMBQPTLAFYVGYXLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR
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Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
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Wermter A.-K., Reichwald K., Platzer M., Preibisch G., Geller F.,
Schaefer H., Remschmidt H., Platzer C., Siefried W.,
Goldschmidt H.-P., Hubes K., Gudermann T., Hinney A., Hebebrand J.,
"Contribution of a nonsynonymous cSNP in the MCHR gene to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MCRI HUMAN STANDARD; PRT; 422 AA.

099705; 096847; 09BV08;

091705; 096847; 09BV08;

10-0CT-2003 (Rel. 42, Last sequence update)

10-0CT-2003 (Rel. 42, Last annotation update)

Melanin-concentrating hormone receptor 1 (MCH receptor 1) (MCHR-1) (MCHR-1) (MCHR) (G protein coupled receptor 24)

(Somatostatin receptor-like protein) (SLC-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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frontal cortex and hypothalamus, lower levels in the liver and

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M. M. M. Molthen R., Wright H.;

M. M. M. Molthen R., Wright H.;

M. M. M. M. Molthen R., Molthen R., Molthen M., Molt
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MEDLINE=2288257; PubMed=12477932;

MEDLINE=2288257; PubMed=12477932;

MISURE=2288257; PubMed=12477932;

MISURE=2288257; PubMed=12477932;

MISURE=2288257; PubMed=12477932;

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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Melanin-concentrating hormone is the cognate ligand for the orphan G-protein-coupled receptor SLC-1.";

Nature 400.261-265(1999).

-I- FUNCTION: Receptor for melanin-concentrating hormone, coupled to both G proteins that inhibit adenyly! cyclase and G proteins that activate phosphoinositide hydrolysis.

-I- SUBCELULAR LOCATION: Integral membrane protein.
-I- TISSUE SPECIFICITY: Highest level in brain, particularly in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 77-422 FROM N.A. MEDILINE: JOHNSON M.P., Lynch K.R., Kolakowski L.F. Jr., Jung B977118; Kolakowski L.F. Jr., Jung B977, Muyyen T., Johnson M.P., Lynch K.R., Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F., "Characterization of a human gene related to genes encoding
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Hervieu G., Dytko G.M., Foley J.J., Martin J., Liu W.S., Park J.,
Ellis C., Ganguly S., Konchar S., Cluderay J., Leslie R., Wilson S.,
Sarau H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roc. Natl. Acad. Sci: U.S.A. 99:16899-16903(2002).
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FEBS Lett. 398:253-258(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCRHODOSEN.

PRINTS; PR01507; MCHRECEPTOR.

PRINTS; PR01507; MCHRECEPTOR.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

PROMITE; PR00262; G_PROTEIN_RECEP_F1_2; 1.

PROMITE; PS00262; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 601751; -
60, 60:0008887; C:integral to plasma membrane; TAS.
60, 60:0004930; F:G-protein coupled receptor activity; TAS.
60; 60:0007204; F:G-protein coupled receptor activity; TAS.
60; 60:0007204; F:neuropeptide receptor activity; TAS.
60; 60:0007204; F:protein calcium ion concentration elevation; TAS.
60; 60:000731; P:feeding behavior; TAS.
60; 60:0007186; P:G-protein coupled receptor protein signalin. .; TV
60; 60:0007185; P:G-protein signaling, adenylate cyclase inhi. .; TV
InterPro; IPR000276; GER_Rhodpsn.
InterPro; IPR004376; MCH_receptor.
InterPro; IPR008361; MCH_receptor.
                                                                     initiator.
CAUTION: Ref.4 and Ref.6 sequences differ from that shown due to
erroneous gene model prediction.
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                                SIMILARITY: Belongs to family 1 of G-protein coupled receptors. CAUTION: It is uncertain whether Met-1, Met-6 or Met-70 is the
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLIAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLONAC. .) (POTENTIAL).
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CYTOPLASMIC (FOTENTIAL).
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EXTRACELLULAR. (FOTENTIAL).
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EMBL; AF490537; AA014670.1; --
EMBL; BT006725; AAR3337.1.1; --
EMBL; Z86090; CAB62043.1; ALT_SEQ.
EMBL; BC001736; AAH01736.1; --
EMBL; U71092; AAC14887.1; --
EMBL; U71092; AAC14887.1; ALT_SEQ.
PIR; JC7080; JC7080; GPR24.
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             HOWARGGEWVFGGPLCTIITSLDTCNOFACSAIMTVMSVDRYFALVOPFRLTRWRTRYKT 150
                                         HOLMGNGVWHFGETMCTLITAMDANSOFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA 229
                                                                                                   289
                                                                                                                               LPLILVCYILILCYTWEMYQQNKDARCCNPSVP-----KQRVMKLTKMVLVLVVVFILS 263
                                                                                                                                              290 FVVITAAYVRIL-----QRMTSSVAPASQRSIRLRTKRVTRIAIAICLVFFVC 337
                                                                                                                                                                                      AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
                                                                                                                                                                                                            Panetra B. Greenwood M. T., Warszynska A., Demchyshyn L.L., Day R., Niznik H.B., Srikant C.B., Patel Y.C.; Niznik H.B., Srikant C.B., Patel Y.C.; Patel Y.C.; Mollik H.B., Srikant C.B., Patel Y.C.; Mollocular cloning, functional characterization, and chromosomal localization of a human somatostatin receptor (somatostatin receptor type 5) with preferential affinity for somatostatin-28.", Mol. Pharmacol. 45:417-427(1994).

FORWING: Receptor for somatostatin-28.", Freeptor is mediated by G proteins which inhibit adenylyl cyclase. Freeptor is mediated by G proteins which inhibit adenylyl cyclase. SUBCELLULAR LOCATION: Integral membrane protein.

FINISUE SPECIFICITY: Prominent in the pituitary and small intestine. Low levels in islets and spleen. Not detected in kidney, pancreas, cerebellum, or cortex.

FINISATTY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                  230 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCIRLPNPDTDLYWFTLYQFFLAFALP
                                                                      151 IRINIGLWAASFILALPVWYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93125499; PubMed=1362243; O'Carroll A.-M., Lolait S.J., Konig M., Mahan L.C.; Molecular cloning and expression of a pituitary somatostatin receptor with preferential affinity for somatostatin-28."; Mol. Pharmacol. 42:939-946(1992).
                                                                                                                                                                                                                                                                                                                                                                             01-UTL-1993 (Rel. 26, Created)
01-FRB-1995 (Rel. 31, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
Somatostatin receptor type 5 (SSSR).
                                                                                                                                                                                                                                                                                                                                                  363 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94195267; PubMed=7908405;
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EMBL; U01152; AAC09011.1; -.
EMBL; X74828; CAA52825.1; -.
PIR; IS7940; IS7940.
                                                                                                                                                                                                                                                                | : :: |
AAQGQLRAVSN 408
                                                                                                                                                                                                                                                 ATEKEINNMGN 334
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                                                                                                                                                                                                                                                                                                                                                   SSR5_RAT
P30938;
                                                                                                                                                                                         264
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17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIM 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 KIVINVXILNLAVADVLEMLGLPFLATQNAVVSYMPEGSFLCRLVMTLDGINQFTSIFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 AFDLTSPDDV-LWYTLYLITT---FFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM---EQPTLAFYVGYYLSICLSYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 WNTSAELL-NKSWNKEFAYQTASVVD--TVILPSMIGIICSTGLVGNILIVFTIIRSRK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL)

N-LINKED (GLCNAC...) (POTENTIAL)

N-LINKED (GLCNAC...) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-palmitoyl cysteine (Potential). 4BD4512960613B4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 35.3%; Score 468.5; DB 1; Length 3 Similarity 35.3%; Pred. No. 3.5e-26; Conservative 70; Mismatches 112; Indels
             FLOUR, PROUGOL; 7tm 1; 1.

PRINTS; PROC237; GFCRHODOPSN.

PROSITE; PSC0237; G-PROTEIN RECEP_F1_1; 1.

PROSITE; PSC0262; G-PROTEIN RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipprotein; Palmitate.

DOMAIN.
                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL) .
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                   7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                6 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 NSCANPLLYGFLSDNFRQSFRKV 318
HSSP, P02699; 1F88.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39971 MW;
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63
73
73
1111
1133
1155
1176-
2221
247
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TRANSMEM
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TRANSMEM
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SEQUENCE FROM N.A.
STRANT=129/SvJ; TISSUB=Liver;
MEDLINE=97444289; PubMed=930621;
Lublin A.L., Diehl N.L., Hochgeschwender U.;
"Isolation and characterization of the gene encoding the type 5 mouse (Mus musculus) somatostatin receptor (msst5).";
                                                                                                                                                                                                                                                                                                                       Baumeister H., Roosterman D., Schafer J., Kreuzer O., Meyerhof W., Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for somatostatin-28. The activity of this receptor is mediated by G proteins which inhibit adenylyl cyclase.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=EALB/c; IISSUE=Liver; Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James R.A.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOTLASMIC (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL)

N.LINKED (GLCNAC. .) (POTENTIAL)

N.LINKED (GLCNAC. .) (POTENTIAL)

N.LINKED (GLCNAC. .) (POTENTIAL)
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR0037; GFCRHODPSN.
PROSITE; PS00237; G_ROTEIN_RECEP_F1_1; 1.
PROSITE; PS02026; G_ROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.
                                                                                                                                                                Moldovan S., Demayo F., Brunicardi F.C.; Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
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1 (POTENTIAL).
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2 (POTENTIAL)
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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V -> VV (IN REF. 1).
YGF -> LWL (IN REF. 2
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EMBL; AF004740; AAB61418.1; -.
EMBL; AF030441; AAB86492.1; -.
EMBL; AF035777; AAB88302.1; ALT_INIT.
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                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                 STRAIN=129/SvJ;
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TRANSMEM
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Length 362;

Score 458.5; DB 1; Pred. No. 1.7e-25;

25.5%;

Query Match Best Local Similarity

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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 RRSERKUTRMVVVVVLVFVGCWLPFFIUNIVNLAFTLDEEPTSAGL--YFFVVVLSYANS
                                                                                                                                                                                                                                                                                               VPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNOFACSAIMTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 DLTSPDDV-LWYTLYLTITT---FFFPLPLILVCYILILCYTWEMYQQNKDARCCNPSVP
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                                                                                              19 SWNKEFAYQTA---SVVD----TVILPSMIGLICSTGLVGNILLVFTIIR-SRKKT
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MEDLINES-3238970; PubMed=8097479;

Corness J.D., Demchyshyn L.L., Seeman P., van Tol H.H.M.,

Srikant C.B., Kent G., Patel Y.C., Niznik H.B.;

A human somatostatin receptor (SSTR3), located on chromosome 22,

displays preferential affinity for somatostatin-14 like peptides.";

FESS Lett. 321:279-284(1993).
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Catarrhini, Hominidae, Homo.
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MEDILINE=93149123; PubMed=1337145;
Yamada Y., Reisine T., Law S.F., Ihara Y., Kubota A., Kagimoto S.Seino M., Seinon Y., Bell G.I., Seño S.,
"Somatostatin receptors, an expanding gene family: cloning and functional characterization of human SSTR3, a protein coupled to
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Indels
103;
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Last annotation update)
type 3 (SS3R) (SSR-28).
Mismatches
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Mol. Endocrinol. 6:2136-2142(1992)
68;
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Mammalia; Eutheria; Primates;
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01-OCT-1993
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B. Miller K.L.G. Frogeward Name Took and the Confidence of Confidence of the Confidence of the Confidence of Confidence of the Confidence of Confidence of the Confidence of Co
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GNILLVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTII 109
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                                                                                                                                                                                                                                                                                                                                                                                                VYSKVIKFKDGVESCAPDLTSPDDVLW---YTLYLTITTFFFPLPLILVCYILILCYTWE 226
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MEDILINE=92108031; PubMed=1346068;
Yamada Y., Post S., Wang K., Tager H.S., Bell G.I., Seino S.;
Yamada dunctional characterization of a family of human and
"Cloning and functional characterization of a family of human and
mouse somatostatin receptors expressed in brain, gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                     CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                             DB 1; Length 418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 LAFYVGYYLSICLSYASSSINPFLYILLSGNFOKRLPQIORRATEK 327
                                                                                                                                                                                                                                          25.4%; Score 456.5; DB 1; Length 32.4%; Pred. No. 2.7e-25; ive 75; Mismatches 128; Indels
                             CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
5 (POTENTIAL).
                                                                                                    6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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S -> T (in dbSNP:229568).
/FTIG=VAR_011853.
                                                                                                                                                                                                                   1227095F801190C4 CRC64;
            2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
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Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992)
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01-UUL-1993 (Rel. 26, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Somatostatin receptor type 1 (SSIR) (SRIF-2).
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  Homo sapiens (Human)
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Best Local Similarity
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SEQUENCE FROM N.A.
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  SSR1 HUMAN
P30872;
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TRANSMEM
DOMAIN
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CARBOHYD
DISULFID
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                                              DOMAIN
TRANSMEM
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MEDLINE-20200451; PubMed=10734105;
A Schwaerzler A., Kreienkamp H.-J., Richter D.;
A Schwaerzler A., Kreienkamp H.-J., Richter D.;
A Schwaerzler A., Kreienkamp H.-J., Richter D.;
A Chan 275:9557-9562(2000).
C Biol. Chem. 275:9557-9562(2000).
C FUNCTION: Receptor for somatostatin with higher affinity for somatostatin-14 than -28. This receptor is coupled via pertussis commander of adenylyl cyclase. In addition is stimulates phosphotyrosine phospharase and Na(+)/H(+) exchanger via pertussis toxin insensitive G proteins.
C SUBUNIT: Interacts with SKB1.
C SUBUNIT: Interacts with SKB1.
C SUBUNIT: Fetal kidney, fetal liver, and adult pancreas, brain, lung, jejunum and stomach.
C SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                         Attaubherg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blate N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blate N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hisheh F.M.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Boraldo M.F., Caranin T.L., Schetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan F.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Saljska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
Lyco. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005894; E:somatostatin receptor activity; TAS.
GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007187; P:G-protein signaling; Coupled to cyclic nucl. .; TAS.
GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. .; TAS.
GO; GO:0007884; P:response to nutrients; TAS.
InterPro: IPR000276; GPCR_Rhodpsn.
Kopatz S.A., Aronstam R.S., Sharma S.V.; "cDMA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (UUN-2003) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                 TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
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                                                                                                                              SEQUENCE FROM N.A.
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148 YKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDD--VLWYTLYLTITT 205
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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MEDLINE=92108031; PubMed=1346068;
Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Seino S.;
"Cloning and functional characterization of a family of human and mouse somatostatin receptors expressed in brain. gastrointestinal tract, and kidney.";
                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-palmitoyl cysteine (Potential). 85C99AFFF339A43D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.0%; Score 449; DB 1; Length 391; 31.3%; Pred. No. 8.6e-25; ive 67; Mismatches 111; Indels
                                                                      1 (POTENTIAL).
CYTOPLAGNIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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01-JUL-1993 (Rel. 26, Last seqn
10-OCT-2003 (Rel. 42, Last anno
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01-DEC-1992 (Rel. 24, Last seq
15-MAR-2004 (Rel. 43, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                             (Rat)
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TRANSMEM
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                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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  Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).

-!- FUNCTION: Receptor for somatostatin with higher affinity for somatostatin with higher affinity for somatostatin-14 than -28. This receptor is coupled via pertussis toxin sensitive G proteins to inhibition of ademylyl cyclase. In addition it stimulates phosphotyrosine phosphatase and Na(+)/H(+) exchanger via pertussis toxin insensitive G proteins.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICTTY: Johnum and stomach.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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N-LINKED (GLCNAC. .) (POTENTIAL).
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BY SIMILARITY.
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31.3%; Pred. No. 8.6e-25;
ive 67; Mismatches 111; Indels
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family; Lipoprotein; Palmitate.
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GO; GO:0005624; C:membrane fraction; IDA.
GO; GO:0005886; C:plasma membrane; IDA.
GO; GO:0004994; F:somatostatin receptor activity; IDA.
GO; GO:0007215; P:glutamate signaling pathway; IDA.
GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
InterPro; IPR00276; GPCR_Rhodpsn.
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391 AA;
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--KITLMVMMVV 277
                                                                       VVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRL 317
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SUBCELDIAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Brain, pituitary, islet, jejunum, stomach,
                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Li X.-J., Forte M., North R.A., Ross C.A., Snyder S.H.;
"Cloning and expression of a rat somatostatin receptor enriched in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRANTE-Wister; TISSUE-Brain;
MEDILINE-92096(11); PubMed=1661599;
MEYERINE W., Paust H.J., Schoenrock C., Richter D.;
Meyerhof W., Paust H.J., Schoenrock C., Richter D.;
"Cloning of a cDNA encoding a novel putative G-protein-coupled
"Cloning of a cDNA encoding a novel putative G-protein-coupled
receptor expressed in specific rat brain regions.";
DNA Cell Biol. 10:689-694(1991).
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODDPSN.
PROSITE; PS00237; GPRRHODDPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1 1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.
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56
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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2 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
133
(POTENTIAL).
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                                                                                                                                                                                                                              318 PQI-----QRRATEKEINNMGNTLKS 338
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EMBL; M97656; -; NOT_ANNOTATED_CDS.
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SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                                                                                                                                                     148 YKTIRINLGLWAASFILALPVWYSKVIKFKDGVESCAFDLTSPDD--VLWYTLYLTTT
                                                                                                                                                                                                                                                               TVAKVVNLGVWVLSLLVILPIVVFSRTAANSDGTVACNMLMPEPAQRWLVGFVLYTFLMG
                                                                                                                                                                                                                                                                                        FFFPLPLILVCYILILCYT-----WEMYQQNKDARCCNPSVPKQRVMKLTKMVLVLV
                                                                                                                                                                                                                                                                                                     VILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLI---
                                                                                                                                                              Gaps
      4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
BY SIMILARITY.
S-PALMILOYI CYSTEINE (POTENTIAL).
S-PALMILOYI CYSTEINE (POTENTIAL).
S-PALMILOYI CYSTEINE (POTENTIAL).
S-PALMILOYI CYSTEINE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                               46;
                                                                                                                                           ; Score 449; DB 1; Length 391;
; Pred. No. 8.6e-25;
67; Mismatches 111; Indels 4
 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILATILY).
SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1994 (Rel. 28, Created)
10-FEB-1994 (Rel. 28, Last sequence update)
11-FEB-1994 (Rel. 43, Last annotation update)
Somatostatin receptor type 2 (SS2R) (SRIF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                             368 AA
                                                                                                                                                                                                                                                                                                                                                                           CRILCLSWMDNAAEEPVDYYATALKS 360
                                                                                                                                                                                                                                                                                                                                                              POI ----- ORRATEKEINNMGNTLKS 338
                                                                                                                           42746 MW;
                                                                                                                                           25.0%;
31.3%;
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
                                                                                                                339
391 AA;
                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                  P34993;
01-FEB-1994
01-FEB-1994
15-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                           BOVIN
DOMAIN
TRANSMEM
                 DOMAIN
TRANSMEM
                                   DOMAIN
TRANSMEM
                                                    DOMAIN
TRANSMEM
                                                                                               CARBOHYD
DISULFID
                                                                                                                LIPID
SEQUENCE
                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                                               318
                                                                                                                                                                                                                                                                                        206
                                                                                                                                                                                                                                                                                                                                                                                335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae;
                                                                               CARBOHYD
                                                                                       CARBOHYD
                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                           T 14
BOVIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstainnthe European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 TSPDDVLWYT---LYLTITTFFFPLFLILVCYILILCYTWEMYQQNKDARCCNPSVPKQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PG-SGAWYTGFIIYAFILGFLVPLTIICLCYLFII-----IKVKSSGIRVGSSKRKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMS
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EXTRACELLULAR (POTENTIAL).

GYOTENTIAL).

GYOTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

S.PALMIALRITY.

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                                                                                                                                                                                                                                                        HSSP, P02699; 1BCJ. ....; ...
InterPro; 1PR00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODPSN.
PROSITE; PS02627; G PROTEIN RECRE F1 1; 1.
PROSITE; PS50262; G_PROTEIN RECREF12; 1.
PROSITE; PS50262; G_PROTEIN TRANSMEMDrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (POTENTIAL)
CYTOPLASMIC (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 89:10267-10271(1992).
-!- FUNCTION: Receptor for somatostatins-14 and -28. This receptor is coupled via pertussis toxin sensitive G proteins to inhibition of adenylary cyclass.
-!- SUBCELLULAR LOGATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Densely expressed in cerebellum and in moderate levels in the amygdala, cortex, striatum, spleen, liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression pattern with that of a somatostatin-14 receptor in rat
                                                                                                                                                                                                                             Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
PSY SMILLARITY.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Wistar; TISSUB=Brain; MbDiINB=33066220; PubMed=1279674; Meyerhof W., Wulfsen I., Schoenrock C., Fehr S., Richter D.; Meyerhof W., Wulfsen I., Schoenrock C., Receptor and comparison Modecular cloning of a somatostatin-28 receptor and comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODDSN.
PROSITE; PS00237; G_PCRHODDSN.
PROSITE; PS00262; G_PROTEIN RECEP_F1_1; 1.
PROSITE; PS026262; G_PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Somatostatin receptor type 3 (SS3R) (SSR-28).
428 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47151 MW;
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STANDARD;
                                                                                                                                                                                                             Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358
428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISSP; P34996; 1DDD.
                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multigene family
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119 ACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFK 178
                                                                                                                                              246 CQWYQAPACQRRRSERRVTRMVVAVVALFVLCWMPFYLLNIVNVVCPLPEEP--AFFGL 303
14 LDPGNASSAWPLDTSLGNASAGTSLA---GLAVSGILISLVYLVVCVVGLLGNSLVIXVV
                                                 60 IR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQF
                                                                                                                                                                                                                  236 CCNPSVP----KQRVMKLIKMVLVLVVVFILSAAPYHVIQLVNLQM---EQPTLAFYVG
                                                                        1 IRHISSPSVISNYILNLALADELFMLGLPFLAAQNAL-SYWPFGSLMCRLVMAVDGINQF
                                                                                                                                                                                               179 DGVESCAFDLISPDDVLWYTLYLITT---FFFPLPLILVCYILILCYTWEMYQQNKDAR
                                                                                                                                                                                                                                                                                                                                            288 YYLSICLSYASSSINPFLYILLSGNFOKRLPQIORRATEK 327
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Query Match

24.6%; Score 441.5; DB 1; Length 4

Best Local Similarity 31.8%; Pred. No. 3.1e-24;

Matches 108; Conservative 73; Mismatches 136; Indels

Gaps

23;

DB 1; Length 428;

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Q8min7 mustela put
Q8mip5 canis famil
Q80113 fugu rubrip
Q80152 fugu rubrip
Q80162 fugu rubrip
Q8mip6 canis famil
Q80116 brachydanio
Q80116 brachydanio
Q701289 carassius a
Q96gg4 mus musculu
Q80wl5 fugu rubrip
Q91k40 mus musculu
Q86yf2 homo sapien
                                                                                                                                                                                                                      May 13, 2004, 16:15:11; Search time 45 Seconds (without alignments) 2383.915 Million cell updates/sec
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1 MNPFHASCWNTSAELLNKSW......QRRATEKEINNMGNTLKSHF 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%.
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                        OM protein - protein search, using sw model
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QB0173
QB0173
QB0173
QB0176
QB
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sp_organelle:*
sp_blage:*
sp_plant:*
sp_vodent:*
sp_virus:*
sp_virus:*
sp_vurtebrate:*
sp_unclassified:*
sp_vurtes:*
sp_vorres:*
sp_vorres:*
sp_vorres:*
sp_prorres:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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1: sp_arches:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                      US-09-913-770B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_archeap:
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
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                                                                                                                                                                                                                                  Run on:
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484.5 468.5 467.5 467.5

464 458.5 456.5

Q8mi04 ovis aries Q95x66 ovis aries Q95yvg0 carassius a Q9ayvg1 carassius a Q6axm7 carassius a Q7tt86 rattus norv Q9gyg7 rus scrofa Q8bq97 mus musculu Q81yd3 homo sapien Q8can5 mus musculu Q8ch75 mus musculu Q8vi70 mus musculu Q8vi69 mus musculu		ace update) stion update) subtype 2 MCH-2R. y Vertebrata; Euteleostomi; lia; Mustelidae; Mustelinae; lia; Mustelidae; Mustelinae; ailer A., Hreniuk D.L., d., Austin C.P., Jiang M.M., d., Kanatani A., c. Subtypes 1 and 2: Species- lk/DDBJ databases. lia. i IEA. c. or activity; IEA.
	NTS	ation subty, Vert dia; Wert dia; W. Y. Ka M. Y. Ka M. J. BA. j IEA. tor ac ceptor i 1.
	IMEN 34	sequence annotation aniata; vissipedia in J., Sai aniata; vissipedia an X.M., ceceptor 6 GenBank, hbrane; lEA. receptor receptor receptor or.
QBMIO4 Q95KG6 Q9PVP9 Q9PVP9 Q9PVP0 Q7TT86 Q9CD5 Q9U14 Q9U14 Q9CH70 Q8CH71 Q8CH71 Q8CH71 Q9CH10 Q9CH10 Q9CH10 Q9CH10 Q9CH11 Q9CGM2 Q9CGM4 Q9CGM	ALIGNMENTS PRT; 340	Created) Last sequence Last annotation Dolecat; Ta; Craniata; Ve A; Craniata; Ve Cuple Receptor Coupled receptor Coupl
		rel. 22, C: el. 22, Licell. 23, Licell. 24, Licell. 24
64 64 64 64 64 64 64 64 64 64 64 64 64 6	; x,	11. 22, 11. 22, 12. 25, 13. 25, 14. 25, 15. 26, 16. 27, 17. 27
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0.0044460000000000000000000000000000000	RELI	TTERMENT TITEMENT TITEMENT TITEMENT TITEMENT TO THE TENDED TO THE TENDE
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4 4 44 446 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 MIN7	Quanto 1.007-2002 (TrEMBLrel. 22, Created) 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) 01-0CT-2003 (TrEMBLrel. 22, Last sequence update) Melanin-concentrating hormone receptor subtype 2 MC Mustela putorius (European polecat). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Carnivora; Fissipedia; Mustelid Mustela. Mustela. Ill SEQUENCE FROM N.A. SEQUENCE FROM N.A. Ten C.P., Sano H., Pan J., Sailer A., Hr Feighner S.D., Palyha O.C., Figueroa D.J., Austin C. Yu H., Ito J., Ito M., Ito M., Guan X.M., Kanatani Sand der Ploeg L.H., Howard A.D.) Van der Ploeg L.H.T., Howard A.D.) "Melanin-Concentrating Hormone Receptor Subtypes 1 (Specific Gene Expression.") Submitted (MAY-2002) to the EMBL/GenBank/DDBJ datab EMBL, AVI12899 AAM51633.1; Geoptor activity; GO; GO:000186; P: Receptor activity; IEA. GO; GO:000186; P: Receptor activity; GO; GO:000186; P: Receptor activity; GO; GO:000186; P: Receptor activity; GO; GO:000186; P: Rhodopsin-like receptor activity; GO; GO:000186; P: Rhodopsin-like receptor protein InterPro; IPR008361; MCHZ. receptor. InterPro; IPR008361; MCHZ. receptor. FRINTS; PR01784; MCHZRECEPTOR. PRINTS; PR01784; MCHZRECEPTOR. PROSITE; PS00237; GPCRHODOPSN.
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MYSLHSSCWNTSAEPLNKSCNKEFAYHTLSILDTXRLPSMIGIICSMGLVGNILIVFTII
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hes 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00001; 7tm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=31033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003
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01-OCT-2003
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                     300
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                                                                                                      09
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                                                                                                                                                        SAIMIVMSVDRYLALVQPFRLTSWRTRYKTIRINLGLWAASFILALPVWYXSKVIKFKDG
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                                                                                                                                                                                                                                                                                                                                     VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS
                                                                                                                                                                                                                                                                                                    VESCAFDLTSPDDVLRYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCYNPS
                                                                                          VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILLILCYTWEMYQQNKDARCCNPS
                                                                      MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Tan C.P., Sano H., Iwaasa H., Pan J., Sailer A., Hreniuk D.L.,

Teighner S.D., Palyha O.C., Figueroa D.J., Austin C.P., Jiang M.M.,

Yu H., Ito J., Ito M., Ito M., Ito M., Kanatani A.,

Van der Ploeg L.H.T., Howard A.D.,

"Melanin-Concentrating Hormone Receptor Subtypes 1 and 2: Species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBNIPS;
QBNIPS;
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Melanin-concentrating hormone receptor subtype 2.
Canis familiaris (Dog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY112659; AAM51852.1; -
GO; GO:0016011; C:integral to membrane; IEA.
GO; GO:0018872; F:receptor activity; IEA.
GO; GO:001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodopsn.
InterPro; IPR008363; MGLZ_receptor.
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        Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.7%; Score 1577; DB 6; Length 3 90.8%; Pred. No. 6.8e-140; ive 13; Mismatches 17; Indels
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330 AA; 37757 MW; 4AF3F85621A1CACB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   INPELYILLSGNFOKRLPQIQRRATEKEINNMGNTLKSHF 340
                                                                                                                                                                                                                                                                                                                                                                                                                      16;
        Query Match
91.7%; Score 1648; DB 6;
Best Local Similarity 91.2%; Pred. No. 1.5e-146;
Matches 310; Conservative 14; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01783; MCHRECEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam, PP00001, 7tm 1, 1.
PRINTS, PR00237, GPCRRHODOPSN.
PRINTS, PR01784, MCH2RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Specific Gene Expression.";
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297; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                          241
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                                                                                                                                            61
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Matches 29
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Q8MIP5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
61 RSRKKTIPDIYICNLAVADLVHIIGMPFLIHQWARGGEWVFGGFLCTIITSLDTCNQFAC 120
                                                                                                                                                                                                                                                                                                                                                                                       241 VPKERVMKLTKMVLVLVAVFILSAAPYHVIQLVNLKWQQPTLAFHVGYYLSICFSYASSS 300
                                                                                 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
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                                                                                                                                                                                                                                              VPKQRVMKLTKMVLVLVVVPILSAAPYHVIQLVNLQMEQPTLAFYVGXYLSICLSYASSS
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                                                                                                                                                                                                             VESCAFDLISPDDVLWYTLYLTITFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fugur rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Neoperygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthoperygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length 331;
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GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:receptor activity; IEA.

GO; GO:0007218; F:receptor activity; IEA.

InterPro; IPR004047; MCHI_receptor.

InterPro; IPR004047; MCHI_receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Logan D.W., Bryson-Richardson R.J., Pagan K.E., Taylor M
Currie P.D., Jackson I.J.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 AA; 36947 MW; 532D0D9C4B74AD1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEWBLrel. 24, Created)
(TrEWBLrel. 24, Last sequence update)
(TrEWBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Melanin-concentrating hormone receptor 1 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 INPFLYILLSGNFOKRLPQIORRATEK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 INPELYIMLSGNFRKRLÞQVQRRVTEK 327
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270 WAPYYULQLIQLSISRPILIFVYLYNAAISLGYANSCINPFVYIVLCETFRKKLVLSVKP 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 FYSLTLYHVESSIRRVK-----RKQSVWARRAIKMYLMVIGLFLICWSPYHVIQVL 267
                  AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFOKRLPQIQRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 IFPTIYGILCSVGVIANGLVIYAVTVCKKKNVSDIYVLNLAIADMLFILVMPFNIHQLVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 GGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 GLWAASFILALPVWVYSKVIKPKDGVESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 LVWLGSFLLTVPVMLYAKV-EQRQNTEVCMMNLDGPEDMYWYTLYQSILGFIIPLIIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYILILCYTWEMYQQNKDARCCNPSVPKQRV--MKLTKMVLVLVVVFILSAAPYHVIQLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 ILPSMIGIICSTGLVGNILIVFTIIRSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]

SEQUENCE FROM N.A.
Logan D.W., Bryson-Richardson R.J., Pagan K.E., Taylor M.S.,
A currle P.D., Jackson I.J.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, Alfelled. A024756.1;
DR GO; GO:00015021; C:integral to membrane; IEA.
GO; GO:0001532; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhddopsin-like receptor activity; IEA.
GO; GO:0001586; P:G-protein coupled receptor protein signalin...;
DR HR000216; GEPRODESI, MCH_receptor.
                                                                                                                                                                                                                                                                                                                                                                     Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Takifugostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLOMEOPTLAFYVGYXLSICLSYASSSINPFLYILLSGNFOKRL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40871 MW; CD97C3DB3AFFC1BB CRC64;
                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.6%; Score 568; DB 13;
39.4%; Pred. No. 4.7e-45;
tive 64; Mismatches 94;
                                                                                                                                                                                                                                   360 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0237; GPCRRHODOPSN.
PRINTS; PRO1783; MCHRECEPOR.
PROSITE; PSO0237; G PROTEIN RECEP 11; 1.
PROSITE; PSS0262; G PROTEIN RECEP 12; 1.
                                                                                                                                                                                                                                                                                                                                  Melanin-concentrating hormone receptor 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353
                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                      (TrEMBLrel. 2 (TrEMBLrel. 2
                                                                                                                       330 AAQGQLRTVSN 340
                                                                                               ATEKEINNMGN 334
                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 112; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=31033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor.
SEQUENCE
                    264
                                                                                               324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                 Q801F2
Q801F2;
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Q8MIP6
ID Q8MI
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IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSP-DDVLWYTLYLTITTFFFP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .; IEA.
                                                                                                   162 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP
                      122 IVIGE-VWGMSVLTIIPVWMYAGLMPLPDGSVACALLLPNPVSDTYWFTLYQFFLAFALP
                                                                            LPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQ---RVMKLTKMVLVLVVVFILSAAP
                                                                                                                                                      YHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 IIMPSVFGTICLLGIVGNSTVIFAVVXKSKLHWCSNVPDIFIINLSVVDLLFLLGMPFMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOWARGGEWVFGGPLCTIITSLDTCNOFACSAIMTVMSVDRYFALVOPFRLTRWRTRYKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lakaye B., Adamantidis A., Coumans B., Zorzi W., Parmentier M., Grisar T., "Cloning of the mouse melanin-concentrating hormone receptor 1 gland promoter characterization."; Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0030273; F:melanin-concentrating hormone receptor acti.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007218; P:neuropepiide signaling pathway; IEA.
InterPro; IPR0004047; MCRI. Receptor.
InterPro; IPR008161; MCH_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Melanin-concentrating hormone receptor 1 alternate form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C8088113F93619A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.7%; Score 569.5; DB 11; 36.7%; Pred. No. 3.3e-45; ive 60; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                         354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEAM, PRO1001, 7tm 1, 1.

PRINTS, PRO1027, GPCRRHODOPSN.

PRINTS, PRO10507, MCHIRECEPTOR.

PRINTS, PRO1783, MCHRECEPTOR.

PROSITE, PSS0262, G_PROTEIN_RECEP_F1_2, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 36.75
                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                          Q8K3M8;
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                     KEINNWGNT 335
                                                                                                                                                                                                                                                                        KVRVNPSTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=129/SvJ
                                                                                                               181
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Q8K3M8
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41 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCSNVPDIFIINLSVVDLLFLLGMPFMI 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . ., IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 FVVITAAYVRIL------QRWTSSVAÞASQRSIRLRTKRVTRTAIAICLVFFVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 HOWARGGEWYFGGPLCTIITSLDTCNOFACSAIMTVMSVDRYFALVOPFRLTRWRTRYKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 HOLMGNGVWHFGETWCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 LPLILVCYILILCYTWENYQQNKDARCCNPSVP-----KQRVMKLTKMVLVLVVVFILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                           Tan C.P., Sano H., Iwaasa H., Pan J., Sailer A., Hreniuk D.L., Feighner S.D., Palyha O.C., Figueroa D.J., Austin C.P., Jiang M.M. Yu H., Ito J., Ito M., Ito M., Guan X.M., Kanatani A., Van der Ploeg L.H.T., Howard A.D.; "Melanin-Concentrating Hormone Receptor Subtypes 1 and 2: Species-Specific Gene Expression."
Chordata, Craniata, Vertebrata, Euteleostomi,
Carnivora, Fissipedia, Mustelidae, Mustelinae,
                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AY112898; AAM51632.1; --
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:melanin-concentrating hormone receptor acti...
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007188; P:neuropeptide signaling pathway; IEA.
InterPro; IPR00276; GPCR Hodosa.
InterPro; IPR004047; MCH1_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.5%; Score 565.5; DB 6; Length 353; 36.3%; Pred. No. 7.8e-45; live 61; Mismatches 114; Indels 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4A489B97EAC85D76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-UTN-2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Melanin-concentrating hormone receptor 1b (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEAM; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHDODOSN.
PRINTS; PR01507; MCHIRECEPTOR.
PRINTS; PR01783; MCHRECEPTOR.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 AA; 38935 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 36.3
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATEKEINNMGN 334
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                                 Mammalia; Butheria;
                                                                                       NCBI_TaxID=9668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Q801F5;
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Q801F5
      임
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                                                                                                                                                                                                                                                                                                                                       Tan C.P., Sano H., Waasa H., Pan J., Sailer A., Hreniuk D.L.,
RA Feighner S.D., Palyha O.C., Figuerca D.J., Austin C.P., Jiang M.M.,
Reighner S.D., Palyha O.C., Figuerca D.J., Austin C.P., Jiang M.M.,
Ru H., Ito J., Ito M., Ito M., Kanatani A.,
Rad der Ploeg L.H.T., Howard A.D.;
Rad van der Ploeg L.H.T., Howard A.D.;
Receptor Subtypes 1 and 2: Species
Specific Gene Expression.";
Specific Gene Expression.";
Specific Gene Expression.";
RML; A7112658; AAMS1851.1; -
CG; GO:0016021; C:integral to membrane; IEA.
RG; GO:0004872; F:receptor activity; IEA.
RG; GO:0004872; F:receptor activity; IEA.
RG; GO:0001584; F:rhodopsin-like receptor activity; IEA.
RG; GO:00001584; F:rhodopsin-like receptor activity; IEA.
RG; GO:00001584; F:rhodopsin-like signaling pathway; IEA.
RITHERPO: IPRO04047; MCHI_receptor.
RITHERPO: IPRO04047; MCHI_receptor.
REPRO: PRO04017 MCHI_receptor.
REPRO: REPRO: REPROSSION MCHI_receptor.
REPRO: REPRO: REPROSSION MCHI_receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 IMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCSNVPDIPIINLSVVDLLFLLGMPFMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTTTFFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 TLVICLIWALSFISITPVWLYARLIPFPGGTVGCGIRDPNPDTDLYWFTLYQFFLAFALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQRVMKLTKMVLVLVVVFILSAAPYHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI
                                                                                                                                                                                      Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 31.5%; Score 566.5; DB 6; Length 353; Local Similarity 37.0%; Pred. No. 6.3e-45; tes 113; Conservative 62; Mismatches 119; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Melanin-concentrating hormone receptor subtype 1 MCH-1R.
Mustela putorius (European polecat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 AA; 39064 MW; 3D8FC5FAF047A83B CRC64;
                                     01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                            Melanin-concentrating hormone receptor subtype Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE, PS50262; G_PROTEIN_RECEP_F1_2; 1.
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PRINTS; PR01507; MCHIRECEPTOR.
PRINTS; PR01783; MCHRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00001; 7tm
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAVSN 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNMGN 334
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211 PLILVCYILILCYTWEMYQQNKDARCCNPSVPKQ----RVMKLTKMVLVLVVVFILSAAP 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 LVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPF 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 NKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVAD 79
                                                                                                                                                                                                                                                                                                                                                                                                152 RINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFPL
                                                                                                                                                                                                                                                                                                                                                                        ILPSMIGIICSTGLVGNILIVFTIIR----SRKKTVPDIYICNLAVADLVHIVGMPFLIH
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Gaps
                                                                                                                                                                                                                                                                                                                                 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.9%; Score 484.5; DB 13; Length 377; 36.8%; Pred. No. 3.4e-37; ive 64; Mismatches 107; Indels 23;
                                                                                                                                                                                                                                                                                        Query Match 30.5%; Score 548.5; DB 13; Length 322; Best Local Similarity 37.6%; Pred. No. 2.8e-43; Matches 109; Conservative 65; Mismatches 97; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Somatostatin-like receptors in goldfish: cloning of four
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
CO; GO:0007218; P:neuropeptide signaling pathway; IEA.
InterPro; IPR000276; GPCE Rhodopsn.
InterPro; IPR0004047; MCHL receptor.
InterPro; IPR008341; MCHL receptor.
Pfam; PP00001; 71ml.; 1.
PRINTS; PR00277; GPCRHODOPSN.
PRINTS; PR01277; MCHIRECEPTOR.
PRINTS; PR01507; MCHIRECEPTOR.
PRINTS; PR01783; MCHRECEPTOR.
PROSITE; PS50262; G_PR0TEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                               322 AA; 35831 MW; D041EBEB841B004E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 AA; 41898 MW; FBF0CE0F022AB148 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last seq
(TrEMBLrel. 25, Last ann
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MEDLINE=22465070; PubMed=12576085;
Lin X., Peter R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carassius auratus (Goldfish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptides 24:53-63(2003).
EMBL; AF472593; AAP68899.1;
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182 TIICVVFFKIL-
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01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSP-DDVLWYTLYLTITTFFFP 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VLMPSIYGVICFVGIIGNCIVIYTIVKKTKFRAQQTVPDIFIFSLCIADLLFLLGMPLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQ----RVMKLTKMVLVLVVVFILSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKR 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Logan D.W., Bryson-Richardson R.J., Pagan K.E., Taylor M.S., Currie P.D., Jackson I.J., Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                         Logan D.W., Bryson-Richardson R.J., Pagan K.E., Taylor M.S., Currie P.D., Jackson I.J.; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY161858; AAO24753.1; -
                                                                                                                           GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0030273; F:melanin-concentrating hormone receptor GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
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328 AA; 36702 MW; 1B41A65641EDADOF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q801F6 PRELIMINARY; PRT; 322 AA. Q801F6; 01-JUN-2003 (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Melanin-concentrating hormone receptor la (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.7%; Score 551.5; DB 1.
37.1%; Pred. No. 1.5e-43;
tive 66; Mismatches 98
                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01503; MCHIRECEPTOR.
PRINTS; PR01783; MCHRECEPTOR.
PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                              InterPro; IPRO00276; GPCR_Rhodpsn.
InterPro; IPRO00406; IQ MHG.
InterPro; IPRO04047; MCHL Teceptor.
InterPro; IPRO08361; MCH_Feceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 37.15
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                Pfam; PF00001; 7tm_
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MCHR1A

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us-09-913-770b-1.rspt

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69; Mismatches 114; Indels
                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                       Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.0%; Score 467.5; 33.1%; Pred. No. 1.4
                                                                                                                                      380
                                                                    294 LSYASSSINPFLYILLSGNFOKRLPQI 320
                                                                                     294 LTYVNSCANPLLYSFLSDNFKRSFQQV 320
                                                                                                                                                          Created)
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                     MEDLINE=20453044; PubMed=10996426;
                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Las 01-JUN-2003 (TrEMBLrel. 24, Las Somatostatin receptor type two.
                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity 33.1
111; Conservative
                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                NCBI_TaxID=7957;
                               235
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Best Local S
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                                                                                                                    RESULT 12
Q9DGQ6
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                                                                                                                                                                                                                                                                                                                                  RSTKWRRPRVAKAVSAAVWAFSFIVVLPVIFSDV---QDTFNSCNMSWPEPRDI-WSTA 210
                                                                    200 YLTITT---FFFPLPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQR--VMKLTYMVL 254
                                                                               VLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVG-YYLSICLSYASSSINPFLYILLSGNF 313
                                                                                                                       60 IR-SRKKTVPDIYICNLAVADLVHIVGMPFL-IHQWARGGEWVFGGFLCTIITSLDTCNQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISTFCLTVMSIDRYMAVVHPIRSARWRRPRVAKVINSMVWALSCLTLFVIIYCDV--- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 KDGVESCAFDLTSPDDVLWYT---LYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDA 234
                               RLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDDVLWYTL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCWNTS-ABLINKS--WNKEFAYQTASVV----DTVILPSMIGLICSTGLVGNILLVFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                           Carassius auratus (Goldfish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes,
Cyptinidae, Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.1%; Score 468.5; DB 13; Length 390; 36.7%; Pred. No. 1.1e-35; ive 60; Mismatches 122; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor; Transmembrane.
                                                                                                                                                                                                                                     01-070-2002 (TrEMBLrel. 21, Created)
01-0708-2002 (TrEMBLrel. 21, Last sequence update)
01-0708-2003 (TrEMBLrel. 24, Last annotation update)
Type five-like somatostatin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0237; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS0038; HIM_1; 1.
G_PDOTCHIN COUDIEd receptor; Receptor; Transsequence 390 AA; 44136 MW; EC12119A4B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                               KOSFRKV 329
                                                                                                                                                 QKRLPQI 320
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Best Local Similarity
Matches 120; Conserv
                                                                                                                              263
                                                                                                           255
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"Molecular cloning and expression of a type-two somatostatin receptor
In goldfish brain and pituliary.",

"Molecular cloning and expression of a type-two somatostatin receptor
In goldfish brain and pituliary.",

Mol. Cell. Endocrinol. 166:75-87(2000).

-!- SUBCELDILAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO PAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

ENEL, AR139597; AAF98367.1; --

--- SIMILARITY: PRECEPTOR activity; IEA.

GO; GO:00016021; C:integral to membrane; IEA.

GO; GO:0001884; F:receptor activity; IEA.

RO; GO:0001884; F:receptor activity; IEA.

GO; GO:0001885; F:receptor activity; IEA.

GO; GO:0001885; F:receptor activity; IEA.

RO; GO:00018
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RCCNPSVPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVG-YYLSIC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 VVVFVICWLPFYVFNVTSVTGTVPTTPVLKSTFDFVVVLGYANSCANPILYAFLSDNFKK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
                                                                235 R-AGLSKRGRSEKKVTRMVVIIVVVFVLCMLPFFIINILNLISTLPENSLMTGIYFLTVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 QTSSVVITFV----YFVVCAVGLCGNALVMYVILRYAKMKTVTNIYILNLAVADVLCMLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTASVVDTVILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 YLTIT---TFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQRVMKLTKMVLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carassius auratus (Goldfish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Carassius.
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MEDLINE=21564205; PubMed=11707075; Badheri-Fam S., Ferraz C., Demaille J., Scherer G., Pfeifer D.; Badheri-Fam S., Ferraz C., Demaille J., Scherer G., Pfeifer D.; Comparative Genomics of the SCNS Region in Human and Fugu rubripes: Conservation of Short Regulatory Sequence Elements within Large
                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 108; Conserv
                                                                       Intergenic Regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193
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                                                                                                                                                                                                                                                                                                                                                                                                                22
                                                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                                                                                                                             53 ILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGG--EWVFGGPLCTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 MYQQNKDARCCNPSVPKQR-VMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 VKVRSSGRRVRATSIRRRKSECKITRMVVIVVAVFVFCWLDFYVLNIVNLLVLLDG-DFR
                                                                                                                                                                                                                                                                                                                                                                                                                6 ASCW-NTSAELL-NKSWNKEFAYQTASVVDT-----VILPSMIGIICSTGLVGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSLDTCNOFACSAIMTVMSVDRYFALVOPFRLTRWRTRYKTIRINLGLWAASFILALPVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 VYSKVIKFKDGVESCAFDLTSPDDVLW---YTLYLTITTFFFPLPLILVCYILILCYTWE
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                      oloci-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
Type-three sometostatin receptor subtype B.
Carassius auratus (Goldfish)
Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
1011—TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Takifugu.
NCBI_TaxID=31033,
                                                                                                                                                                                                                                                                                                                                                                                        37;
                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 452;
                                                                                                                                                                                                                                                                           new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 GLYYFVVVLSYANSCANPILYGFLSDNFKRGFRKALCRSSRRVENQD 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 VGYYLSICLSYASSSINPFLYILLSGN----FQKRLPQIQRRATEKE 328
                                                                                                                                                                                                                                                             Lin X., Peter R.E.; "Somatostatin-like receptors in goldfish: cloning of four
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                       50776 MW; DBA53D223D5B16D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                        81; Mismatches 116;
              330 SFONVLCLKRVGGLDEIERSDSRQBRIRMVNDVMS 364
                                                                                                                                                                                                                                                                                                                                                               26.0%; Score 467.5; DB 1
32.6%; Pred, No. 1.6e-35;
--LPQIQRRATEXEINNMGNTLKS
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                                                                                    Ā
                                                                                    452
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MEDLINE=22465070; PubMed=12576085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel, 20, 01-MAR-2002 (TrEMBLrel, 20, 01-JUN-2003 (TrEMBLrel, 24, Somatostatin receptor 2.
                                                                                                                                                                                                                                                                                                                                                                           32.6%;
                                                                                                                                                                                                                                                                                                               EMBL; AF510109; AAP68900.1;
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 32.6'
Matches 113, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                  Peptides 24:53-63(2003)
                                                                                                                                                                                                                                                                                                                                        452 AA;
                                                                                                                                                                                                                                                                                          receptors."
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                    Q7T2S8
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                                                           RESULT 13
Q7T2S8
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Genomics 78:73-82(2001).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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O'Carroll A.-M.;

"Cloning, sequence and tissue distribution of the gene encoding a mouse somatostatin subtype 5 receptor.";

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

-! SUBCELLUIAR LOCATION; INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-! SIMILARITY; BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
                                                            25.8%; Score 464; DB 13; Length 370; 33.1%; Pred. No. 2.8e-35; cive 64; Mismatches 114; Indels 40
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Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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94 VTNVYILNIAVADVLFMLGLPFLATQNA-VSYWPFGSFLCRLVMTLDGINQFTSIFCLMV 152
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GO; GO:0016812; F:receptor activity; IEA.
GO; GO:0001584; F:receptor activity; IEA.
GO; GO:0001584; F:receptor activity; IEA.
GO; GO:0001186; P:G-protein coupled receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
PROSITE; PR00227; GPCRHODPSN.
PROSITE; PS00227; GPROTEIN RECEP F1 1; 1.
PROSITE; PS00227; GPROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane.
SEQUENCE 385 AA; 42489 MW; SEC1140BF09FCEB5 CRC64;
                                                                                                                                                                                                                                                                                                                                     SWNKEFAYOTA---SVVD-----TVILPSMIGIICSTGLVGNILIVFTIIR-SRKKT 66
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Job time: 46 secs
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Best Local Similarity 35.45
Matches 112; Conservative
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1798
1 MNPFHASCWNTSAELLNKSW......QRRATEKEINNMGNTLKSHF 340
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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1586107 Total number of hits satisfying chosen parameters: seq length: 0 seq length: 200000000 Minimum DB & Maximum DB &

1586107 segs, 282547505 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* Geneseq 29Jan04:* geneseqp2000s:* geneseqp1980s:* genesedp1990s:* geneseqp2001s:* geneseqp2004s:* Database

Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Human AXO Human G-p Human mel Human mel Human G p Human G p Human G p Monkey MC Monkey me Monkey MC Human G-p Ferret MC Cat melan Canine MC Dog melan G protein Human TGR Human MCH Human mel Aab23540 Human Aau25610 Human Amino Description Aao27467 1 Abw00463 1 Abb07986 1 Abp81746 | Abw01467 | Ade24736 | Aae31490 Ade24746 Abw01469 Ade24756 Aab68893 Aau04381 Aae14795 Aae35562 Aam51568 Abw01468 Aae18650 Aau97733 Aae31492 Aae31491 SUMMARIES AAE31492 AAE14795 5562 AAM51568 AR18650 7467 4AB68428 AAE3149 AAE3 Query Match Length DB 1792 1765 1765 1763 1763 1763 1784 1689 1588 1588 1798 Score 1798 1798 1798 1798 1798 1798 1798 Result Š.

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## ALIGNMENTS

RESULT 1

G-protein coupled receptor; SLT; antiallergic; antirheumatic; antidiabetic; nootropic; neuroprotective; antiinflammatory; neuroleptic; hypotensive; nervous system disorder; hormonal disorder; schizophrenia; inflammatory diseases; cardiovascular disease; Alzheimer's disease; allergy; rheumatism; sodium intolerance; diabetes; hypertension. Human G-protein coupled receptor SLT protein sequence. AAB23540 standard; protein; 340 AA. (first entry) 02-JAN-2001 AAB23540; AAB23540

18-FEB-2000; 2000WO-JP000927. 99JP-00125768 99JP-00041336 WO200049046-A1. 19-FEB-1999; Homo sapiens 24-AUG-2000. 

Shintani (TAKE ) TAKEDA CHEM IND LID. Terao Y, WPI; 2000-543749/49. N-PSDB; AAA90097. 06-MAY-1999; Watanabe T,

G protein coupled receptor protein SLT, DNA encoding it and antibodies recognizing it, useful for treatment and diagnosis of e.g. neurological diseases

Claim 1; Fig 1; 108pp; Japanese.

This invention relates to a G-protein coupled receptor protein, SLT of human origin. The nucleotide and protein sequences are given in the specification. The invention includes expression vector containing SLT encoding polynuclectide sequences, host cells transformed with the vectors, and methods for preparing SLT through the culturing of the transformants. Also included are anti-SLT antibodies, SLT ligands and methods for their identification. SLT exhibits antiallergic, antidiabetic, nootropic, neuroprotective,

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antiinflammatory, neuroleptic, and hypotensive activity. The G protein coupled receptor protein SLT, the DNA encoding it and its antibodies can be used for the diagnosis and treatment of diseases with which SLT is associated, such as disorders of SLT expression. These include nervous system disorders, hormonal disorders, inflammatory diseases, cardiovascular diseases, and liver/gall bladder/pancreas diseases (such as Alzheimer's disease, schlizophrenia, allergies, rheumatism, sodium intolerance, diabetes and hypertension). The present sequence represents
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100.0%; Pred. No. 5.3e-196;
iive 0; Mismatches 0;
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                                                                                                                                              SLT protein sequence of the invention
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23-FEB-2000; 2000US-0184303P.
23-FEB-2000; 2000US-0184304P.
23-FEB-2000; 2000US-0184305P.
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Best Local Similarity 100.
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Sequences AAU25554-AAU25616 represent human G-protein coupled receptor (GPCR) polypeptides of the invention. The proteins and their associated DNA sequences can be used to identify compounds which bind to GPCR polypeptides and in screening for compounds that modulate GPCR activity By screening a human subject for the presence of mutations in GPCR activity GPCR-related disorder or a genetic predisposition can be diagnosed. The esquences can also be used for treatment and prevention of mental disorders such as schizophrenia, attention deficit disorder, anxiety, depression, dementia and bipolar disorder, neurological disorders such as Huntington's disease, Parkinson's disease and Tourette's syndrome, metabolic disorders such as obesity, anorexia and type 2 diabetes, cardiomyopathy and atherosclerosis, viral infections caused by HIV and
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                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid encoding a new G-protein coupled receptor polypeptide for detecting receptor modulators that can treat mental disorders, such as schizophrenia, anxiety, depression, or obesity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1798; DB 4; Length 340; 100.0%; Pred. No. 5.3e-196;
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                                                                                 2000US-0213861P.
2000US-0217369P.
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2000US-0218337P.
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                                                 13-MAR-2000; 2
03-APR-2000; 2
23-JUN-2000; 2
11-JUL-2000; 2
                                                                                                                         11-JUL-2000;
14-JUL-2000;
                                                                                                                                                             20-JUL-2000;
                                                                                                                                                                                                                                 Vogeli G,
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AAB68428 standard; protein; 340 AA

RESULT 3 AAB68428 ID AAB6

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The invention relates to a novel protein comprising a fully defined 340 amino acid sequence, or the sequence contealing one or more amino acid substitutions, deletions or insertions. The protein shows melanin concentrating hormone (MCH) receptor activity. It is a G protein coupled receptor that binds to MCH. The protein is used to find agents to treat obesity, cachexia, anorexia nervosa and hyperphagia. The present sequence is a human MCH receptor polypeptide of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein with melanin concentrating hormone receptor activity, for
                                                                                                                                                                                                                                                                                                                                                                                                                           cachexia; anorexia nervosa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            finding antagonists for treating obesity and eating disorders.
                                                                                                                                                                                                                                                                                                                                                                                              Human, melanin concentrating hormone, MCH, MCH receptor, G protein coupled receptor, obesity, cachexia, anorexia rhyperphagia, anorectic, antianorectic.
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                                                                                                          100.0%; Score 1798; DB 4;
100.0%; Pred. No. 5.3e-196;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                           Human melanin concentrating hormone receptor #1.
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da T, Saito
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(HELI-) HELIX RES INST.
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                                                                                                                                            G-protein coupled receptor, HG67; MCH-R2; weight loss; obesity; stress; melainin concentrating hormone receptor; cancer; pain; sexual dysfunction; weight gain; hypertension; dyslipidemia; cardiovascular disease; gall stone; osteoarthritis; cancer; diabetes; anorexia; AIDS; wasting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
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                                                                                                      G-protein coupled receptor HG67.
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; Pred. No. 5.3e-196;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Howard AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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2000US-0188977P.
2000US-0198029P.
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(BANY ) BANYU PHARM CO LTD.
                                                              (first entry)
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N-PSDB; AAF85372.
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Best Local Similarity
Matches 340; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                  Human, AXOR21; G-protein coupled receptor; anorectic; antidiabetic; cytostatic; antiasthmatic; antiparkinsonian; cardiant; hypertensive; costeopathic; antianginal; cerebroprotective; antiulcer; antiallergic; antimigraine; antiemetic; tranquiliser; antimanic; gene therapy; vaccine; cancer; neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel G-protein coupled receptor polypeptide, AXOR21, useful for treating obesity, diabetes, eating disorders such as anorexia and bulimia, hypertension, osteoporosis, angina pectoris and myocardial infarction.
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                                                                  300
                                                                                     241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMSPTLAFYVGYYLSICLSYASSS 300
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                       VESCAFDLISPDDVLWYILYLIITFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS
VESCAFDLISPDDVLWYTLYLITITFFFPLPLILVCYILLLCYTWEMYQQNKDARCCNPS
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24-AUG-1999;
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                                                                                    RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC
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                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                              receptor; GPCR; hRUP27; agonist;
                   Indels
                                                                                                                                                                                                                                                                               301 INPFLYILLSGNFOKRLPQIORRATEKEINNMGNTLKSHF 340
                                                                                                                                                                                                                                                              INPFLYILLSGNFOKRLPQIORRATEKEINNMGNTLKSHF 340
         Pred. No. 5.3e-196;
                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           Human G-protein coupled receptor, hRUP27.
                                                                                                                                                                                                                                                                                                                                            AAU04381 standard; protein; 340 AA.
100.08; Pr. 0;
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99US-0171901P.
99US-0171902P.
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2000US-0189258P.
2000US-0189259P.
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2000US-0196078P.
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                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
         Similarity 100.
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14-MAR-2000; 2
14-MAR-2000; 2
10-APR-2000; 2
10-APR-2000; 2
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12-MAY-2000;
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17-NOV-1999;
23-DEC-1999;
23-DEC-1999;
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                                                                                                                                                                                              The sequence represents a human G-protein coupled receptor (GPCR), hRUP27. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vito and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased
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                                                                                                Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILLICYTWEMYQQNKDARCCNPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1798; DB 4;
; Pred. No. 5.3e-196;
0; Mismatches 0;
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                                                                                                                                                                         Claim 77; Page 125-126; 160pp; English
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Best Local Similarity 100.
Matches 340; Conservative
                                                2001-355616/37.
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                                                                   N-PSDB; AAS07954
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The invention describes a method of screening for compounds or their salts that can change affinity of melanin-concentrating hormone (MCH) with its G protein-coupled orphan receptor protein, SLT. The screened MCH receptor agonists are useful as appetite-stimulating agents and its antagonist for preventing or treating obesity e.g. malignant mastocystosis, exceptous obesity and hyperinsulinar obesity, and also for treating sexual function disorders, overpowering intermittent pains, still borns, uterus rupture, premature birth and Prader Willi syndrome. This is the amino acid sequence of the G protein-coupled orphan receptor
                                                                                                                                                                                                                                   obesity,
                                                                                                                                                                                                     Screening for compounds or salts which alter affinity of melanin-
concentrating hormone with its receptor to provide agonists as appetite-
stimulating agents and its antagonist for preventing or treating obesity
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                                       04-JUL-2001; 2001WO-JP005809
                                                                     05-JUL-2000; 2000JP-00208254
                                                                                                                                                            WPI; 2002-164552/21.
N-PSDB; ABK10848, ABK10852.
                                                                                                                                                                                                                                                    uses a protein or hormone.
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                                                                                                                                                                                                                                                                                                                                                            New isolated G-protein couple receptor polypeptide, termed TGR, for diagnosis and treatment of diseases such as renal failure, nephritis, hypothyroidism, diabetes insipidus, and disturbances of thirst and sleep.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (GPCR)
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                                                    sleep disturbance; temperature regulation; blood pressure; hypothalamus;
 Human; TGR342; receptor; G-protein coupled receptor; GPCR; TGR; TGR-associated disorder; signal transduction; renal failure, nephritis; hypothyroidism; hypogonadism; retinitis pigmentosa; growth disorder; diabetes insipidus; hyperprolactinaemia; thirst disturbance; appetite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII
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100.0%; Pred. No. 5.3e-196;
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22-DEC-2000; 2000US-0257656F.
12-JAN-2001; 2001US-025177P.
28-MAR-2001; 2001US-029954P.
29-MAR-2001; 2001US-0280696P.
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                                                                                                                                                                                                                                                                       (TULA-) TULARIK INC
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Best Local Similarity
Matches 340; Conserv
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                                                                 circadian rhythm
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                                                                                                                 WO200242458-A2
                                                                                         Homo sapiens
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Human; melanin-concentrating hormone type 2 receptor; MCH-2R;
INPFLYILLSGNFOKRLPQIQRRATEKEINNMGNTLKSHF 340
                                                        INPFLYILLSGNFOKRLPQIQRRATEKEINNMGNTLKSHF
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31-MAY-2001; 2001US-0294747P

& CO INC. PHARM CO LTD.

MERCK

WPI; 2003-047225/04.

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N-PSDB; AAD48423

body weight.

2002WO-US016702

28-MAY-2002;

05-DEC-2002

Disclosure; Col 44; 26pp; English.

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Conservative

Query Match Best Local Similarity Matches 340; Conserv

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181

241

301 301

Sequence 340 AA;

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The invention relates to a melanin concentrating hormone type I receptor (MCHIR) deficient mouse whose genome comprises an alteration in one or both MCHIR alleles, where the alteration substantially reduces expression of a functional MCHIR. The invention also relates to a method of measuring the affect of a compound on a MCHIR deficient mouse and measuring one or more phenotypes associated with MCHIR activity e.g. hyperphagic activity, body weight, locomotor activity, the methods and composition of the present invention are useful for screening of compounds that are further used as a research tool and for treating weight loss or weight gain, reducing pain, stress, anxiety, and treating weight loss or weight gain, reducing pain, stress, anxiety, and treating cancer, sexual dysfunction, diabetes, locomotor deficits, fatigue or sleep disorders. The present sequence is human melanin concentrating hormone type 2 receptor (MCH2R) used in a method of the
                                                                                                                                                                                                                                                                                                                               MCHIR deficient mouse with an alteration in one or both alleles, useful for screening of compounds as a research tool and for achieving useful effects for locomotor activity, stress, anxiety, fatigue, circadian
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Pred. No. 5.3e-196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 30-31; 35pp; English.
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100.0%; Pre
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                                                                                                                                22-MAR-2001; 2001US-0278061P
                                                                                     19-MAR-2002; 2002WO-US008413
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N-PSDB; AAD36796.
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WO200277168-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel melanin-concentrating hormone type. 2 receptor (MCH-2R) proteins and polymucleotides encoding such proteins. ACH-2R is a G-protein coupled receptor that responds to MCH and it distinct from MCH-1R. Sequences of the invention are useful in measuring and monitoring body weight. The present sequence is human MCH-2R protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Melanin concentrating hormone type 2 receptor; MCH2R; hyperphagic; hypophagic; body weight; locometor activity; stress; anxiety; sleep disorder; fatigue; circadian rhythm; energy metabolism; pain; cancer; sexual dysfunction; diabetes; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ő
                                                                                                                                                                                                                                                                                                                    2 receptor useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human melanin concentrating hormone type 2 receptor (MCH2R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INPFLYILLSGNFOKRLPQIQRRATEKEINNMGNTLKSHF 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INPFLYILLSGNFOKRLPQIQRRATEKEINNMGNTLKSHF 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1798; DB 6; 100.0%; Pred. No. 5.3e-196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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AAE14795 standard; protein; 340

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to truncated melanin-concentrating hormone (MCH) analogue peptide active at melanin-concentrating hormone-2 receptor (MCH-2R), or its labelled derivative or salt, useful for increasing weight or appetite in a subject. The peptide is useful for screening for a compound able to bind MCH-2R. It is useful for increasing weight or appetite in a subject having an MCH-2R. It is useful for measuring the ability of a compound to decrease weight or appetite in a subject having MCH-2R. It is useful for measuring the ability of a subject having word and word appetite in a subject having MCH-2R. It is useful to screen for MCH agonists, to explore differences between MCH-1R and MCH-2R and between the presence of MCH-1R and MCH-2R. The present sequence is human MCH-2R protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                    Novel truncated melanin-concentrating hormone analog peptide active at melanin-concentrating hormone-2 receptor, or its labeled derivative or salt, useful for increasing weight or appetite in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDFHASCWNTSAELLNKSWNKEPAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILLLCYTWEMYQQNKDARCCNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VESCAPDLTSPDDVLWYILYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                    Melanin-concentrating hormone-2 receptor; MCH-2R; appetite; MCH-1R; melanin-concentrating hormone; MCH; receptor; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1798; DB 6; Length 340; 100.0%; Pred. No. 5.3e-196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                 Human melanin-concentrating hormone-2 receptor (MCH-2R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INPFLYILLSGNFOKRLPQIQRRATEKEINNMGNTLKSHF 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 16; Page 58; 30pp; English.
                                                                                                                                                                                                                          28-MAY-2002; 2002WO-US016513.
                                                                                                                                                                                                                                                             31-MAY-2001; 2001US-0294806P.
 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity ....
Matches 340; Conservative
                                                                                                                                                                                                                                                                                                (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-201270/19.
                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAD54241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 340 AA;
                                                                                                                                                        WO200297037-A2.
                                                                                                                       Homo sapiens
17-JUN-2003
                                                                                                                                                                                           05-DEC-2002.
                                                                                                                                                                                                                                                                                                                                  Bednarek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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Introduction relates to those foundament metalling control for the main frequents of main frequence of main frequence is made massuring the change in weight for treating disorders accompanied by medical main main frequents of massuring main frequents of main frequence of main frequence of the main main melanin-concentrating hormone (hMCH) type 2 receptor (MCH-2R) against which the peptides of the invention are specifically not targeted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
                                                                                                                                                                                                                                                                                                                                                                   Human, melanin-concentrating hormone, hMCH; MCH type 1 receptor; MCH-1R; MCH-1R agonist, anti-HIV; anabolic; immunomoulator; increasing weight; increasing appetite, weight loss disorder; anorexia; AIDS; wasting; cachexia; frail elderly disease; food intake; hypothalamus neuronal cell body; lateral hypothalamus perikaryon; zona inertia; orexigenic; MCH type 2 receptor; MCH-2R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New optionally substituted truncated human melanin-concentrating hormone (hWCH) peptides are hMCH-1 agonists, useful for increasing appetite/weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNPFHASCWNISAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to novel truncated human melanin-concentrating
                                                                                                                                                                                                                                                                                                   Human melanin-concentrating hormone type 2 receptor (MCH-2R) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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100.0%; Pred. No. 5.3e-196;
ive 0; Mismatches 0;
                                                                           AAO27467 standard; protein; 340 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 20; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JAN-2003; 2003WO-US000241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JAN-2002; 2002US-0347191P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 340; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-646040/61.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                       16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bednarek MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-2003
                                                                                                                                                   AA027467;
RESULT 12
                                       AA027467
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                                                                                                                                                                                                                                                                     MNPFHASCWNTSABLLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII
                                                                                                                                                                                                                                                                                                                                            RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 SAIMIYWSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VESCAFDLISPDDVLMYTLYLTITTFFFPLPLILVCYILLLCYTWEMYQQNKDARCCNPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS
                                                                                                                                                                                                                  1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGLICSTGLVGNILLVFTII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel seven transmembrane domain receptors, designated 65499 or 58875. The 65499 and 58875 polypeptides can be
                                                                                        Length 340;
                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane receptor, 58875 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INPFLYILLSGNFOKRLPOIORRATEKEINNMGNTLKSHF
                                                                                    Score 1798; DB 7;
Pred. No. 5.3e-196;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB07986 standard; protein; 340 AA
                                                                                                                   Best Local Similarity 100.0%; P. Matches 340; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 8; 132pp; English
                                                                                           100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABL41165, ABL41166.
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                                 Sequence 340 AA;
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                                                                                                                                                                                                                                   VESCAFDLISPDDVLMYTLYLITTFFFPLPLILVCYILLCYTWEMYQQNKDARCCNPS 240
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RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
                                                                                                                                                                                                                                                                                                                    VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, G protein-coupled receptor; GPCR; HGPRBMY9; therapy; brain; lung; colon; testes; gastrointestinal; reproductive system; asthma; diabetes; nootropic; gynaecological; Alzheimer's disease; neuroprotective; cancer;
                                                                                                            SAIMTVMSVDRYFALVQPFRLTRWRIRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG
                                                             SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVXSKVIKFKDG
                                                                                                                                                                                                                                                                                                                                                         VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cacace A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  INPFLYILLSGNFOKRLPQIQRRATEKEINNMGNTLKSHF 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human G protein-coupled receptor (GPCR), HGPRBMY9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ramanathan CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABW00463 standard; protein; 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Fig 2; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2000; 2000US-0235709P.
16-JAN-2001; 2001US-0261775P.
02-AUG-2001; 2001US-0309625P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-2001; 2001US-00964923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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MINTIER G./
RAMANATHAN C S
HAWKEN D R.
CACACE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feder JN, Mintier G,
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N-PSDB; AAD61085.
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Homo sapiens.

receptor.

22-MAY-2003

(FEDE/)
(MINT/) I
(RAMA/) I
(HAWK/) I

15-JAN-2004

ABW00463;

ABW00463

Homo sapiens.

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expressed by standard recombinant methodology. The polypeptides, encoding polymucleotides and modulators are useful for controlling G protein coupled receptor-related disorders, and as a novel diagnostic target and therapeutic agent in treatment and diagnosis of 65499 or 58875 mediated of sorders such as cellular proliferative and differentiative disorders (e.g., osteoporosis, rickets), haematopoietic disorders (such as chronic myelogenous leukemia acute promyeloid leukemia,) bone metabolism as chronic myelogenous leukemia acute promyeloid leukemia,) garders (e.g., ischaemic heart disease, myocardial infarction, etc), endothelial cell disorder (e.g., psoriasis, Grave's disease), hrain disorders (e.g., multiple sclerosis, Parkinson's disease), hormonal disorders (diabetes mellitus, hyperthyroidism,), immune disorders (including autoimmune diseases such as rheumatoid arthritis, osteoarthritis,), liver disorders, viral diseases such as heumatoid arthritis, osteoarthritis,), liver disorders (e.g., pain associated with surgery cor chest pain,), metabolic disorders (obesity, cachexia,). The 65499 or chest pain,), metabolic disorders (besity, cachexia,). The 65499 or chest pain,), metabolic markers. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the human 58875 protein
          8x80999999999999888
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Sequence 340 AA;

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120
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                                                                                                                                                                                                                                                                               VESCAPDLISPDDVLWYILYLITITFFFPLELLVCYILLLCYIWEMYQQNKDARCCNPS
                                                                                     MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII
                                                                                                                                  RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC
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                                                                  1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII
                                                                                                                                                            RSRKKTVPDIYTCNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC
                                                                                                                                                                                                                                                              VESCAFDLTSPDDVLMYTLYLTTTTFFFPLPLILVCYILLCYTWEMYQQNKDARCCNPS
                                    Gaps
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Score 1793; DB 5; Length 340;
Pred. No. 2e-195;
                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                             INPFLYILLSGNFOKRLPQIQRRATEKEINNMGNTLKSHF 340
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                                    Mismatches
                                  0;
99.78;
                                     Conservative
 Query Match
Best Local Similarity
                                    Matches 339;
                                                                                                                                    61
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ABP81746 standard; protein; 340 (first entry) 04-MAR-2003 ABP81746; RESULT 15

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9 9 120 180 180 240

Human G protein-coupled receptor SLT/MCH2 protein SEQ ID NO:666.

Alzheimer's disease, atherosclerosis, infection; osteoarthritis; allergy, osteoporosis, cardiomyopathy; inflammation, Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis, anxiety; depression; schizohrenia; dementia; memory loss; mental retardation; epilepsy; asthat, tuberculosis; obesity, nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; G protein-coupled receptor, GPCR, antigenic peptide, gene therapy; of protein-coupled receptor modulator, antibody, immune-related disease, growth-related disease; cell regeneration-related disease; LDS; cancer; immunological-related cell proliferative disease; autoimmune disease; 

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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acid secribed: (1) am assay for the detection of a particular G cadds. Also described: (1) am assay for the detection of a particular G complex cand (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in Gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing the GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, immunological-related diseases, call giseases, or autoimmune diseases, immunological-related diseases, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarchitis, osteoarchis, cancer, cardiomyopathy, chronic and acute disease, parkinson's disease, multiple solerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory ancer; cannon control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABR91675 to ABP82018, which are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC
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99.7%; Pred. No. 2.6e-195;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 1, 523pp; English.
                                                                                                                                                                                                                                                                                           (LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                      Brown JP;
                                                                                                                                                                                                                                   19-DEC-2000; 2000US-0257144P.
                                                                                                                                                                           19-DEC-2001; 2001WO-US050107
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                                                                                                                                                                                                                                                                                                                                                      Burmer GC, Roush CL,
                                                                                                                                                                                                                                                                                                                                                                                                              2003-046718/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases.
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ses 339; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABZ42591
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                                                        WO200261087-A2
                                                                                                                   08-AUG-2002
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241 VPKQXVMKLTKOVLVVVVILLSAAPYHVIQLVNLQMEQPTLAFYVGYVLSICLSYASSS 300

БÞ ò d

Search completed: May 13, 2004, 16:18:27 Job time : 61 secs

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3
                                                                                                                                                         May 13, 2004, 16:17:22; Search time 22 Seconds (without alignments) 797.856 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Ap
Sequence 6, Ap
Sequence 16,
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Sequence 8, A
Sequence 7, A
Sequence 12,
                                                                                                                                                                                                                                                                                                                                 1 MNPFHASCWNTSAELLNKSW......QRRATEKEINNMGNTLKSHF 340
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Sequence
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1. /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

3. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-170-496D-52
US-09-478-601-2
US-09-478-601-2
US-09-170-496D-192
US-07-816-283-2
US-07-816-283-2
US-07-816-283-2
US-08-417-103-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hits satisfying chosen parameters:
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US-09-218-467B-2
PCT-US95-16472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389414 segs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1798
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No.
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Sequence 8, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 17, Appli Sequence 17, Appli Sequence 5, Appli Sequence 5, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 6, Appli Sequence 7, Appli Sequence 6, Appli Sequence 7, Appli	•		• v				Length 340; Indels 0; Gaps 0;	CSTGLVGN LIVFT   60                        ICSTGLVGN LIVFT   60	GGPLCTIITSLDTCNQFAC 120 		YTWEMYQQNKDARCCNPS 240	AFYVGYYLSICLSYASSS 300
US-07-816-283-8 US-08-417-103-8 US-08-1411-859-3 US-08-387-707-9 US-08-387-707-9 US-08-120-6011B-9 US-08-120-6011B-9 US-08-181-271A-17 US-08-188-275A-5 US-09-113-426-5 US-09-151-199-5 US-09-151-199-5 US-09-151-199-5 US-08-405-271A-22	ALIGNMENTS		12368 e P.	S/09/ -14 /165,	/ 100,37 3 /198,02 8 S Versi		Score 1798; DB 4; ; Pred. No. 1.4e-158; 0; Mismatches 0;	AYQTASVVDTVILPSMIG 	VGMPFLIHQWARGGEWVF                 VGMPFLIHQWARGGEWVF	RLTRWRTRYKTIRINLGLWAASF 	ITTEFFPLPLILVCYILILC 	vpilsaapyhviolvnlomeoptlafyw
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2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		RESULT 1 US-09-712-3	Sequence ; Patent N ; GENERAL N ; GENERAL N ; APPLICAL ; APPLICAL	APPLICA TITE REI FILE REI CURRENT CURRENT PRIOR A	PRIOR PROSE	TYPE: TYPE: ORGANI S-09-712-	Query Mat Best Loca Matches	ζό qα	Qy	Qy Db	ço, qo	٨٥

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EARLIER FILING DATE: 1998-12-31
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ORGANISM: Rattus norvegicus
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ORGANISM: Rattus norvegicus
               NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                       Best Local Similarity 36.7
Matches 114; Conservative
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329 AAQGQLRTVSN 339
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                                                                                                                                                                                                                                                       APPLICANT: Nagorny, Raise APPLICANT: Nagorny, Raise APPLICANT: Nagorny, Raise APPLICANT: Wilson, Amy E. TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof FILE CONVENTION: Receptor (MCH1) And Uses Thereof FILE REPERRANCE: 57453/JPW/JHB CURRENT APPLICATION NUMBER: US/09/224,426 CURRENT FILING DATE: 1998-12-31 NUMBER OF SEQ ID NOS: 15 SOFTWARE: Patentin Ver. 2.0 - beta SEQ ID NO 4 LENGTH: 353
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Sequence 4, Application US/09478601
Serient No. 6221616
GENERAL INFORMATION:
APPLICANT: Salon, John A.
APPLICANT: Salon, John A.
APPLICANT: Majorny, Raisa
APPLICANT: Wilson, Amy E.
TITLE OF INVENTION: DAM Encoding A Human Melanin Concentrating Hormone TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
FILE REPERENCE: 574532\DPW
CURRENT PAPLICATION NUMBER: US/09/478,601
CURRENT PILING DATE: 2000-01-06
EARLIER APPLICATION NUMBER: 09/224,426
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                                                           301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
                                                                                                                                               US-09-224-426-4
; Sequence 4, Application US/09224426
; Patent No. 6221613
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APPLICANT: Salon, John A
APPLICANT: Laz, Thomas M .
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ORGANISM: rat
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US-09-478-601-4
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APPLICANT: Salon, John A.
APPLICANT: Salon, John A.
APPLICANT: Nagorny, Raisa
APPLICANT: Wilson, Amy B.
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
TITLE OF INVENTION NUMBER: US/09/478,602
CURRENT FILING DATE: 2000-01-06
EARLIER PRILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 15
SEQ ID NOS: 15
SEQ ID NOS: 15
SEQ ID NOS: 201

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31.7%; Score 569.5; DB 3; Length 36.7%; Pred. No. 6.1e-45; rive 60; Mismatches 114; Indels
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161 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 220
151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
                                                                                                                                                           210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP-----KQRVMKLTKMVLVLVVVFILS 263
                                                                                                                                                                                          221 FVVITAAYVRİL------QRMISSVAPASQRSIRLERTKRVIRTALAICLUVFFVC 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQUENCE 2. Application US/09218467B
Patent No. 636226
GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: BLILS, CATHERINE
APPLICANT: HALSEY, WENDY
ITILE OF INVENTION: 11cby Genomic Sequence
FILE REFERENCE: GP-50010
CURRENT FILICA DATE: 2001-06-22
CURRENT FILICA DATE: 2001-06-22
CURRENT FILICA DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASESEO for Windows Version 3.0
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US-09-218-467B-2
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                                                  221 FVVITAAYVKIL------QRMTSSVAPASQRSIRLRTKRVTRIAIAICLVFFVC 268
                                                                                                             210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP-----KQRVMKLTKMVLVLVVVFILS 263
                                                                                                                                                                                                 264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
                                                                                                                                                                                                                              269 WAPYYVIQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 328
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                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-984-288-2
) Sequence 2, Application US/08984288
) Farent No. 6033872
) GENERAL INFORMATION:
APPLICANT: BERGSMA, DERK
APPLICANT: BERGSMA, DERK
TITLE OF INVENTION: NOVEL HUMAN 11CB SPLICE V
TITLE OF INVENTION: ARIANT
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: RATHURR & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
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APPLICATION NUMBER: US/08/984,288
FILING DATE: 03-DEC-1997
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,763
FILING DATE: 11-DEC-1996
ATTORNEY/AGRET INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
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TELECOMMUNICATION INFORMATION:
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TELEX: 846169
INPORVATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
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amino acid
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Matches 113;
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ELLIS, CATHERINE
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             APPLICANT:
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31.5%; Score 565.5; DB 5; Length
Best Local Similarity 36.3%; Pred. No. 1.6e-44;
Matches 113; Conservative 61; Mismatches 114; Indels
                                                                                                            ADDRESSEE: SmithKline Beecham Corporation/Corporate ADDRESSEE: Intellectual Proper STREET: P. O. Box 1539-UW2220 CITY: King of Prussia STATE: Pennsylvania
                                                                                                                                                                                                                 ZIF: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16472
                                          Catherine E
: Human Somatostatin Receptor
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
TELEPAX: 610 270 5090
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
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NAME: Sutton, Jeffrey A
REGISTRATION NUMBER: 34,028
GENERAL INFORMATION:
APPLICANT: Bergsma, Derk J
APPLICANT: Ellis, Catherine i
TITLE OF INVENTION: Human Son
NÜMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: SMILUKLINE Beecl
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MOLECULE TYPE: protein
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CLASSIFICATION:
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US-08-602-809-2
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90 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLLGMPFMI 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PREJUCTOR OF THE COMPONENT OF THE COMPUTER: IBM COMPONENT OF SOFTHARE: FRSISED for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/602,809 FILING DATE: 13-JUN-1997
HUMAN SOMATOSTATIN-LIKE ECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 15-DEC-1995
APPLICATION NUMBER: US 08/357,675
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23,031
P50277
                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: PS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 601-407-0700
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19482-0980
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610-407-0701
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MOLECULE TYPE: protein
                                                                                           NUMBER OF SEQUENCES:
TITLE OF INVENTION:
TITLE OF INVENTION:
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RESULT 9 US-09-170-496D-52

Sequence 2, Application US/08602809 Patent No. 6008012 GENERAL INFORMATION: APPLICANT: BERGSMA, DERK

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91 HOWARGGEWVFGGPLCTITTSLDTCNOFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
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                                                                                   91 HOWARGGEWVFGGPLCTIITSLDTCNOFACSAIMTVMSVDRYFALVOPFRLTRWRTRYKT 150
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APPLICANT: Salon, John A.
APPLICANT: Salon, John A.
APPLICANT: Salon, John A.
APPLICANT: Nagorny, Raisa
APPLICANT: Wilson, Amy E.
TITLE OF INVENTION: BNa Encoding A Human Melanin Concentrating Hormone;
TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
FILE REFERENCE: 57453 \ JUPW
CURRENT APPLICATION NUMBER: US/09/478,601
CURRENT FILING DATE: 2000-01-06
EARLIER PILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VOR: 2.1
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                            151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP
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Patent No. 6221616
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Best Local Similarity
Matches 113; Conservat
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US-09-478-601-2
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APPLICANT: Salon, John A
APPLICANT: Salon, John A
APPLICANT: Laz, Thomas M
APPLICANT: Laz, Thomas M
APPLICANT: Laz, Thomas M
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
FILE REPERENCE: 57453/JPW/HDM
CURRENT APPLICATION NUMBER: US/09/224,426
CURRENT PILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0 - beta
SEQ ID NO
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; Pred. No. 1.7e-44;
61; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                 31.5%; Score 565.5; DB 4; 36.3%; Pred. No. 1.6e-44; tive 61; Mismatches 114;
                                                  APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Cor
TITLE OF INVENTION: No. 6555339-Endogenous, Cor
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
Sequence 52, Application US/09170496D
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36.3%;
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Best Local Similarity 36.3%
Matches 113; Conservative
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13; Conservative
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AAQGQLRAVSN 388
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US-09-224-426-2
                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                        GENERAL INFORMATION:
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Best Local Simi
Matches 113;
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                                                                                                                                                                                                                                               SEQ ID NO 52
LENGTH: 402
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US-09-224-426-2
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90 IIMPSVEGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLLGMPFMI 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFOKRLPQIQRR 323
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                                                                                                                                                                                                                                                               Length 402;
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MEDIUM TYPE: Floppy disk
COMPUTER: IRW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBRR: US/07/816,283
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APPLICANT: Yamada, Yuichiro
APPLICANT: Yamada, Yuichiro
APPLICANT: Yamada, Yuichiro
APPLICANT: Senino, Susumu
TITLE OF INVENTION: SCMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: PO Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/07816283
Patent No. 5436155
GENERAL INFORMATION:
SOFTWARE: Patentin version 3.1
SEQ ID NO 192
LENGTH: 402
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NAME: McDaniel, C. Steven
TELECOMMUNICATION INFORMATION
TELEPHONE: 713-787-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
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COUNTRY: USA
77210
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                                                                                                            ; TYPE: PRT
; ORGANISM: HOMO
US-09-170-496D-192
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TOPOLOGY:
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US-09-170-496D-192
US-09-170-496D-192
Sequence 192, Application US/09170496D
Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0046
FILE REFERENCE: AREN-0046
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
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Fatent No. 6291195
GENERAL INFORMATION:
APPLICANT: Salon, John A.
APPLICANT: Laz, Thomas M.
APPLICANT: Wilson, Amy E.
APPLICANT: Wilson, Amy E.
TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
FILE REPRENCE: 574537\JPW
CURRENT APPLICATION NUMBER: US/09/478,602
CURRENT FILING DATE: 2000-01-06
FERLIER APPLICATION NUMBER: 09/224,426
EARLIER FILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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                                                                                     398 AAQGQLRAVSN 408
                                  324 ATEKEINNMGN 334
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ORGANISM: Homo sapiens
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Matches 113; Conserv
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US-09-478-602-2
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US-08-417-103-10
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                                                                                                                                                                                                                                                          VYSKVIKFKDGVESCAFDLTSPDDVLW---YTLYLITTFFFFLPLILVCYILLLCYTWE 226
                                                                                                                                            9
                                                                                                                                  227 MYQQNKDARCCNPSVPKQR--VMKLTKMVLVLVVVFILLSAAPYHVIQLVNLQM---EQPT
                                                                                                                                                                                              61 GNSLVIYVVLRHTASPSVTNVYILNLALADELFWLGLPFLAAQNAL-SYWPFGSLMCRLV
                                                                                                               1 MNPFHASCWNTSAELLNKS--WNKEFAYQTAS------VVDTVILPSMIGIICSTGLV
                                                                                  Gaps
                                                                                 31;
                                                   Length 418;
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                                                                                 Indels
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                                                     DB 1;
                                                     25.4%; Score 456.5; DB 1;
llarity 32.4%; Pred. No. 2.1e-34;
Conservative 75; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
CORRESPONDENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
FILING DATE: 05-ARR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARCD:144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Texas
COUNTRY: United States of America
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08417103
Patent No. 572329
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (512) 418-3000
TELEFAX: (512) 474-757
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
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        protein
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                                                                   Best Local Similarity
Matches 112; Conserv
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         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-417-103-10
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US-07-816-283-10
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231 VKVRSAGRRVWAPSCQRRRRSERRVTRMVVAVVALFVLCWMPFYVLNIVNVVCPLPEEFP- 289
                                                                                                                                                                                                                                                                                                                                       170 VYSKVIKFKDGVESCAPDLTSPDDVLW---YTLYLTITTFFFPLPLILVCYILILCYTWE 226
                                                                                                                                                                                                                                                                                                                                                                                                                     227 MYQQNKDARCCNPSVPKQR--VMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM----EQPT 281
                                                                                                                                                                                                                        GNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTII 109
                                                                                                                                                                                                                                                     61 GNSLVIYVVIRHTASPSVTNVYILNLALADELFMLGLPFLAAQNAL-SYWPFGSLMCRLV 119
                                                                                                                                                                                                                                                                                                          110 TSLDTCNOFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVW 169
                                                                                                                                                                     ----VVDTVILPSMIGIICSTGLV
                                                                                                    Gaps
                                                                                                  Indels 31;
                                                         Length 418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 LAFYVGYYLSICLSYASSSINPFLYILLSGNFOKRLPQIORRATEK 327
                                                         25.4%; Score 456.5; DB 1;
32.4%; Pred. No. 2.1e-34;
tive 75; Mismatches 128;
                                                                                                                                            1 MNPFHASCWNTSAELLNKS--WNKEFAYQTAS
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Job time : 24 secs
                                          Query Match
Rest Local Similarity 32.**
protein
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(without alignments)
9211.159 Million cell updates/sec
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/ cgn2 _ 6/ ptodata/2/pubpna/US10B_PUBCOMB.seq
/ cgn2 _ 6/ ptodata/2/pubpna/US10B_PUBCOMB.seq
/ cgn2 _ 6/ ptodata/2/pubpna/US10 _ NEW PUB.seq:
/ cgn2 _ 6/ ptodata/2/pubpna/US10 _ NEW PUB.seq:
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/prodatea/2/pubpna/USO9E_PUBCOMB.seq
/prodatea/2/pubpna/USO9_NEW_PUB.seq-
/prodatea/2/pubpna/USO9_NEW_PUB.seq-2/prodatea/2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW_PUB.seq-2/pubpna/USO9_NEW
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/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq
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prodata/2/pubpna/USO7_NBW_PUB.seq:
prodata/2/pubpna/PCTUS_PUBCOMB.seq:
prodata/2/pubpna/USO8_NBW_PUB.seq:
prodata/2/pubpna/USO8_PUBGOMB.seq:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2947324 segs, 2269024515 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                             OM nucleic - nucleic search, using sw model
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SHIMMADIES

	Description	Sequence 1, Appli	Sequence 1, Appli	Sequence 39, Appl	Sequence 9, Appli	Seguence 4, Appli	Sequence 57, Appl	Sequence 6, Appli	Sequence 3, Appli	Sequence 665, App	Sequence 37, Appl	Sequence 5, Appli	Sequence 37, Appl	Sequence 33, Appl	Sequence 1, Appli
	ΩI	US-09-990-940-1	US-09-964-923A-1	US-10-321-807-39	US-10-332-082-9	US-10-332-082-4	US-09-791-932-57	US-09-971-269-6	US-09-971-269-3	US-10-225-567A-665	US-10-309-515-37	US-10-291-990-5	US-10-126-764-37	US-10-309-515-33	US-10-291-990-1
	DB	10	10	15	17	17	10	10	10	15	15	15	15	15	15
	Query Match Length	1023	1023	1023	1023	1035	1965	1023	1278	1330	1023	1023	1023	1023	1023
de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	8.66	8.66	99.8	96.6	96.6	96.6	96.2	96.2
	Score	1023	1023	1023	1023	1023	1023	1021.4	1021.4	1021	987.8	987.8	987.8	984.6	984.6
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Sequence 33, Appl Sequence 35, Appl Sequence 36, Appl Sequence 38, Appl Sequence 6, Appl Sequence 78, Appl Sequence 49, Appl Sequence 11, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 61,	m
	US-09-865-478 US-09-899-73 US-10-341-75 US-10-029-31 US-09-826-50 US-09-826-50 US-10-309-51
1023 1023 1023 1023 1023 1023 1023 1033 104 1038 1038 1038 1038 1038 1038 1038 1038	
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0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	, ) W W 4 4 4 4 4 4 • 80 0 0 H G W 4 10

## ALIGNMENTS

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US-09-990-900-10.

Sequence 1, Application US/09990940

Publication No. US20030027252A1

GENERAL INFORMATION:

APPLICANT: Tian, Hui

APPLICANT: Cuter, Jiagang

APPLICANT: Cuter, Jian, Hui

APPLICANT: Cuter, Gene

APPLICANT: Cuter, Jamila S.

APPLICANT: Talarik Inc.

TIALOR INVENTION:

APPLICANT: An. Songalu

BRIOR APPLICATION NUMBER: US 60/25,841

PRIOR FILING DATE: 2001-01-22

PRIOR FILING DATE: 2001-01-32

PRIOR FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 54

PRIOR FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 54

SOFTWARE: PATENTIN VONS: 51

ATER: DAA

TYPE: DAA

TYPE
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961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
                                                                                                                                                                                                                                                              | GENERAL INFORMATION:
| APPLICANT: FEDER, U. N. |
| APPLICANT: FEDER, U. N. |
| APPLICANT: MINTIER, G. |
| APPLICANT: MINTIER, G. |
| APPLICANT: MANNATHAN, C. S. |
| APPLICANT: HAWKEN, D. R. |
| APPLICANT: CACACE, A. |
| APPLICANT: CACACE, A. |
| TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPREMY9, TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPREMY9, TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND TESTES |
| TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND TESTES |
| TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND TESTES |
| CURRENT PELLICATION NUMBER: 60/309,625 |
| PRIOR FILING DATE: 2001-09-26 |
| PRIOR PELLING DATE: 2001-01-16 |
| PRIOR PELLING DATE: 2000-09-27 |
| NUMBER OF SEQ ID NOS: 69 |
| SOFTWARE: PATENTIN VET: 2.1 |
| SEQ ID NOS: 69 |
| SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGGTAGATACAGTCATCCTCCCTTCCATG 120
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                                                                                                                                                                                                        Sequence 1, Application US/09964923A Publication No. US20030096300A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-923A-1
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Best Local Similarity
Matches 1023; Conserv
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; OTHER INFORMATION: melanin-concentrating hormone receptor 2 (MCHr2) US-09-990-940-1
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                                                               Query Match 100.0%; Score 1023; Best Local Similarity 100.0%; Pred. No. 0; Matches 1023; Conservative 0; Mismatches
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; Remaining Prior Application data removed - See File Wrapper or PALM.	NUMBER OF SEQ II SOFTWARE: Patent SEQ ID NO 39 LENGTH: 1023	ens 100.0%; Score	Best Local Similarity 100.0%; Pred. No. 0; Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps	OY 1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60	AAITAAAGAGITITGCITATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG	121	Db 121 ATTGGGATTATCTGTTCAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180 Oy 181 AGATCCAGGAAAAAAACAGTCCCTGACATCTTGCAACCTGGCTGTGGCTGATTG 240	181 AGATCCAGGAAAAAACGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGTTTG	Oy 241 GTCCACATAGATGGAATGCCTTTTCTTATTCACCAATGGSCCCGAAGGGGGGGGGG	301 TITGGGGGGGCCCTCTCGCCACCACACTCCCTGGATACTTGTAACCAATTTGCTGT	Db 301 TTTGGGGGCCTCTCTGCACCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360	361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA	AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 42	Oy 421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCGCT 480	Qy 481 TCCTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAATTTAAAGACGGT 540  bb 481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCAATTTAAAGACGGT 540	Qy         541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCTGACGATGTACTCTGGTATACACTTTAT 600           -	Qy 601 TIGACGATAACAACTITITITTCCCTCTACCCTTGATTITGGTGTGCTATATTITAATT 660	Qy 661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720  Db 661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720	CY 721 GTACCAAAACAGAGAGAGATGAAGATGACAAAGATGGTGGTGGTGGTGGTAGTCTTT 780 Db 721 GTACCAAAACAGAGAGTGATGAAGATGGAAAGATGGTGCTGGTGGTGGTGGTGTTT 780	OY 781 AICCTGAGTGCTGCCCTTATCATGTGATACAACTGGTGAACTTACAGAATGGAACAGCCC 840  DD 781 AICCTGAGTGCTGCCCTTATCATGTGATACAACTGGTGAACTTACAGAACAGCCC 840	Qy 841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900	
	DD 481 ICCITIATICCIGGCATIGCCIGICIGGGICIACAGGICATCAAATTIAAAGGIC 540 QY 541 GITGAGAGIIGIGGCIIIIGAATTIGACATCCCCIGACGAIGIACICIGGGATACACTITAI 600 DD 541 GITGAGAGIIGIGCIIIIGAIIIGACAICCCCIGACGAIGIACICIGGIAIACACTITAI 600	OY 601 TTGACGATAACAACTTTTTTTTCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660	661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT	DD 661 ITATGCIALACTIGGGAGATGTCACAGAATAAGGATGCCAGATGCCAGATCCCAGT 720 Qy 721 GTACCAAAACAGAGAGTGATGAAAGATGACAAAGATGGTGCTGGTGGTGGTGTTT 780	GGTAGTCTTT	781	OY 841 ACACTGGCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCGGCTATGCCAGCAGC 900	CCAAATC	901 AIIAACCCIIIICICIACAICCIGCIGAGIGGAAAIIICCAGAAACGICIGCCI 961 CAAAGAAGGGGACTGAGAAAGAAATCAACAATATGGGAAAACACTCTGAAATCA	961 CAAAGAAGAGCGACTGAGAAAGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 102	Oy 1021 TAG 1023	Db 1021 TAG 1023	RESULT 3	US-10-321-807-39 ; Sequence 39, Application US/10321807 ; Publication No. US20030166148A1 ; GREEPA, INFORMATION	-	; IIILE OF INVENTION: No. USZ0030156148A1-Endogenous, Constitutively Activated Human G ; TITLE OF INVENTION: Receptors ; FILE REFERENCE: ARENOOS6 ; CURRENT APPLICATION NUMBER: US/10/321,807	CURRENT FILING DATE: 2002-12-16; PRIOR PEDLICATION NUMBER: US/09/714,008; PRIOR FILING DATE: 2000-11-16; PRIOR APPLICATION NUMBER: 09/170,496		FILING DATE: APPLICATION N FILING DATE: APPLICATION N		FILING DATE: APPLICATION N FILING DATE: APPLICATION N	; PRIOR FILING DATE: 2000-02-11

481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT	601 TIGAGGATAAGAACTITITITITICCCTCT 661 TTAIGCTATACTIGGGAGAIGTAICAACA 661 TTAIGCTATACTIGGGAGAIGTAICAACA 661 TTAIGCTATACTIGGGAGAIGTAICAACA 721 GTACCAAACAGAGAGATGATGACTIGAC 721 GTACCAAACAGAGAGTGATGAAGTIGAC 781 ATCCTGAGTGCTGCCCCTTATCATGTGAT 781 ACCTGAGTGCTGCCCCTTATCATGTGAT 781 ACATGGCCTTCTATGTGAGTTATACCT 841 ACATGGCCTTCTATGTGGGTTATTACCT 901 ATTAACCCTTTCTCTATGTGGGTTATTACCT 901 ATTAACCCTTTTCTCTATGTGGGTTATTACCT 901 ATTAACCCTTTTCTCTATGTGGGTTATTACCT 901 ATTAACCCTTTTCTCTATGTGGGTTATTACCT 901 ATTAACCCTTTTCTCTATGTGGGTTATTACCT 901 ATTAACCCTTTTCTCTATGTGGGTTATTACCT 901 ATTAACCCTTTTCTCTATGTGTGTGTGTGTGTGTGTGTGT	AGAAGGAATCAATATGGAAACACTCTGAATCACACTTTAAACTTTTTTTT	Sequence 4, Application US/10332082	core red. Mism GTTGG
OY 901 ATTAACCCTTTTCTCTACATCCTGAGGAAATTTCCAGAAAGGTCTGCCTCAAATC 960	SULT 4  10-332-082-9  Sequence 9, Applica Sequence 9, Applica Sepuence 9, Applica SERERAL INPORMATION APPLICANT: MORI, M APPLICANT: HARADA APPLICANT: HARADA APPLICANT: SHING APPLICANT: SHING APPLICANT: SHING TITLE OF INVENTION FILE REPRENCE: 27 CURRENT APPLICATION PRIOR FILING DATE: PRIOR FILING D	LENGTH: 1023   TYPE: DNA	1 AIGAATCCATTTCATGCATCTTGTTGGAACCCTCTGCGGACTTTTAAACAATCCTGG 61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGGTGGTAGATACCGGACTTTTAAACAATCCTGG 61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGGTGGTAGATACAGTCATCCTCCCTTCCATG 121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGTAGATACCTCATTGTATTCACTAAATA 121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTAAATA 121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTAATAT 181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGG	0y         241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGAGG

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Sequence 57, Application US/09791932
Publication No. US20030003451A1
                          GENERAL INFORMATION:
APPLICANT: Vogeli, Gabriel
APPLICANT: Parodi, Luis A.
APPLICANT: Hiebsch, Ronald is A.
APPLICANT: Lind, Peter
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RESULT 6 US-09-791-932-57

APPLICANT: Woodsl. Gabriel
APPLICANT: Modell, Gabriel
APPLICANT: Hebsofh, Ronald R.
APPLICANT: Hids Peter
APPLICANT: Hids Wood, Linda S.
TITLE OF INVENTION: NO. US2030003451Alel G Protein-Coupled Receptors Cross-Referer
CURRENT APPLICANTON WOMER: US/09/791,932
CURRENT APPLICANTON WOMER: US/09/184,305
REIOR FILING DATE: 2000-223
REIOR APPLICATION WOMER: CS00-223
REIOR PELING DATE: 2000-7-11
REIOR APPLICATION WOMER: CS00-7-11
REIOR APPLICATION WOMER: CS00-7-11
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REIOR APPLICATION WOMER: CS00-7-11
REIOR APPLICATION WOMER: CS00-1-14
REIOR PELING DATE: 2000-0-1-1
REIOR PELING DATE: 2000-0-1-1
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ORGANISM: Homo sapiens
US-09-791-932-57 Query Match Best Local Similarity Matches 1023; Conserv SOFTWARE: 장_> 업

; SEQ ID NO 6 ; LENGTH: 1023 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-971-269-6 ; US-09-971-269-6 ; OLEY WATCH Guery Match Best Local Similarity 99.9%; Pred. No. 0; Matches 1022; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 1022; Conservative 0; Mismatches 0; Gaps 0;  OY 1 ATGRATICGATTTTCATGCATCTTTCAAAAACTTTTTAAAAAAAAAA	Db 1 ATGANTCCATTTCATGCAACATTCTGCAACATTTTAAACAATCCTGG 60  Qy 61 AATAAAGAGTTTGCTTATCAAACTGCTGGTGGTAGATACAGTCATCCTCCCTTCCATG 120  Db 61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120  Qy 121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGAACATCCTCCTTCCATGTAATA 180	Db 121 ATTGGGATTATCTATCAACAGGCTTGCTATTGCTATTGTATTTACTATAATA 180  Qy 181 AGATCCAGGAAAAAACGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGTTTG 240  Db . 181 AGATCCAGGAAAAAACGTCCCTGACATCTATACCTGCAACGTGTGGCTGTTTG 240  Qy 241 GTCCACATAGTTGGAAATGCCTTTTTTTTTTTATTCACAATGGGCCCAAGGGGAGAGTGTGTTG 300	Db 241 GTCCACATGGAATGCCTTTTTTTTTTTTTGATGGGGGGGG	361 421 421	QY 481 TCCTTTATCCTGGCATTGCCTGTGGGTCTTATGAGGTCATCAAATTTAAAGACGGT 540  Db 481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTGGAAGTTAAAGACGGT 540  QY 541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCTGACGATGTACTCTGGTATACACTTTAT 600  Db 541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCTGACGATGTACTCTGGTATACACTTTAT 600	601 601 661	661 721 721 781		QY 901 ATTAACCCTTTCTCTACATCCTGCTGAAATTTCCAGAAACGTCTGCCTCAAATC 960
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Db 628 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 687  Qy 541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600  bb 688 GTTGAGAGTTGTGCTTTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 747  Qy 601 TTGACGATAACAACTTTTTTTTTCCCTTACCCTTGATTTTGGTATTTTAATT 660  TABLE TTGACGATAACAACTTTTTTTTTTTCCCTTACCCTTGATTTTTGGTATTTTAATT 660  TABLE TTGACGATAACAACTTTTTTTTTTTCCTTACCCTTGATTTTTGGTGTATTTTAATT 660	61 TTATGCTATACTTGGGAATGTATCACAGAATAAGGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCCAGATGCCCAGATGCCCAGATGCCCAGATGCCCAGATGCCCAGATGCCCAGATGCCCAGATGCCCAGATGCCCCAGATGCCCCAGATGCCCCAGATGCCAGATGCCAGAGATGCCAGATGCCAGAGATGCCAGAGATGCCAGAGATGCCAGAGATGCCCCCTAATCACAGATGCTGCCTGC	RESULT 9  US-10-25-567A-665  Sequence 665, Application US/10225567A  PUBLICARIE No. US2030113798A1  GENERAL INFORMATION  APPLICANT: LifeSpan Biosciences  APPLICANT: Brown, Joseph P.  APPLICANT: Brown, Joseph P.  TITLE OF INVENTION: MATIENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED R.  FILE REPERRACE: 1320-4-4  CURRENT APPLICATION NUMBER: 60/257,144  PRIOR APPLICATION NUMBER: 60/257,144  PRIOR APPLICATION NUMBER: 60/257,144  PRIOR APPLICATION NUMBER: 60/257,144  CURRENT FILMS DATE: 2000-12-19  NUMBER OF SEQ ID NOS: 2222  SOFTWARE: Patentin version 3.1  SEQ ID NO 665  CORGANISM: Homo sapiens  US-10-225-667A-665  QUETY MATCH  DEST LOCAL SIMIlarity 99.8%; Pred No. 2.2e-314; Indels  ON TYPE DATE: CONSERVATION OF THE STANDARD AND AND AND AND AND AND AND AND AND AN
QY         961 CAAAGAAGAAGGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACATT 1020           Db         961 CAAAGAAGGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTT 1020           QY         1021 TAG 1023           Db         1021 TAG 1023           Db         1021 TAG 1023	RESULT 8  US-09-371-269-3  Sequence 3, Application US/09971269  Publication No. US2030148281A1  GENERAL INFORMATION: Maria A.  APPLICANT: Milennium Pharmaceuticals, Inc.  APPLICANT: Glucksmann, Maria A.  TITLE OF INVENTION: GR499 AND USES THEREOF  FILE REFERENCE: MP100-414PTRM  TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS AND USES THEREOF  FILE REPERENCE: MP100-414PTRM  CURRENT APPLICATION NUMBER: US 60/237,700  PRIOR APPLICATION NUMBER: US 60/237,700  NUMBER OF SEQ ID NOS: 20  SEQ ID NO 3  LENGTH: 1278  TYPE: DNA  TYPE: DNA  ORGANISM: Homo sapiens  FEATURE:  COATION: (148) (1170)  Guery Match  Best Local Similarity 99.9%; Pred. No. 2.2e-114;  Matches 1022; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	1 ATGANTCCATTTCATGCAACTTTGTTGGAACTCTTGCCGAACTTTTAAACAATCCTGG 60  148 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 207  20 AATAAAGAGTTTGCTTATCAACTGCCAGTGTGGTAGATACATCCTCCCTTCCATG 267  20 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACATCCTCCCTTCCATG 267  21 ATTGGGATTATCTGTTCAAACTGCCAGTGTGGTAGATACAGTCATCATCATGATA 180  22 ATTGGGATTATCTGTTCAACAGGGCTGGTGGTAGATACAGTCATCATTAATA 327  24 ATTGGGATTATCTGTTCAACAGGGCTGGTGGTAGATACAGTCATTGTATTCACTATAATA 327  25 AATTGGGATTATCTGTTCAACAGGGCTGGTTGGCTACCTATTGTATTCACTATAATA 327  26 AATTGGGATTATCTGTTCAACAGGGCTGGTTGGCTACCTATTGTATTCACTATAATA 327  27 ATTGGGGATTATCTGTTCAACAGGGCTGGTTGGCTACTGTATTCACTATAATA 327  27 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCTACTGTATTCACTATAATA 327  28 AGATCCAGGAAAAAACAGTCCCTGACATCTATACCTGCAACTGGTGGTGTATTG 340  29 AGATCCAGGAAAAAACAGTCCCTGACATCTATACCTGCAACTTGGTGGTGGTTG 360  20 AGTCCAACAGTTGGAATGCCTTTTCTTATTCACCAATCTGTAACCAATTTGCCTGT 507  20 AGTCCAACAGTTGGAATGCCTTTTCTTATTCACCAATCTGTAACCAATTTGCCTGT 507  20 AGTCCAACAGTTGAATGAGTTGTAATCACACTCTGTAACCAATTTGCCTGT 507  20 AGTCCCAACAGTTGAATGAGTGTGGAACACTTTGCACCTTTTGGACCAATTTGCCTGT 507  20 AGTCCCAACAGTTGAATGAGTGTGGAACACTTTGCACCTTTTGGACCACTTTTTTTT

RECEPTORS

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TYPE: DNA
; ORGANISM: Macaca fascicularis
US-10-309-515-37
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Best Local Similarity 97.8%;
Matches 1001; Conservative
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APPLICANT: Krause, James B.
TITLE OF INVENTION: Melanin Concentrating Hormone Receptors
FILE REFERENCE: NOO.2102C1
CURRENT APPLICATION NUMBER: US/10/309,515
CURRENT APPLICATION NUMBER: 60/284,835
PRIOR PILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 10/126,764
PRIOR FILING DATE: 2002-04-18
NUMBER: OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
SEQ ID NO 37 Length Indels Score 987.8; DB 15; Pred. No. 5.3e-304; 0; Mismatches 22; 721 661 à g à

721

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US-10-309-515-37 Sequence 37, Application US/10309515 Publication No. US20030114644A1 GENERAL INFORMATION: APPLICANT: Bennett Kinrade, Michele APPLICANT: Brodbeck, Robbin M.

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; Publication No. US20030166834A1
; GENERAL INPORMATION:
; APPLICANT: Bennett Kinrade, Michele
; APPLICANT: Brodbeck, Robbin
; APPLICANT: Excuse, James
; TITLE OF INVENTION: MELANIN CONCENTRATING HORMONE RECEPTORS
; FILE REFERENCE: NOO. 2102
; CURRENT APPLICATION NUMBER: US/10/126,764
; CURRENT FILING DATE: 2002-04-18
; RICR APPLICATION NUMBER: 60/284,835
PRIOR FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 37
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Pred. No. 5.3e-304;
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; ORGANISM: Macaca fascicularis
US-10-126-764-37
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PUBLICANT: Bennett Kinrade, Michele

APPLICANT: Bennett Kinrade, Michele

APPLICANT: Bennett Kinrade, Michele

APPLICANT: Bennett Kinrade, Michele

APPLICANT: Waters, Stephen

APPLICANT: Krause, James E.

TITLE OF INVENTON: Monkey and Canine Melanin Concentrating Hormone Rece

CURRENT APPLICATION NUMBER: US/10/291,990

CURRENT APPLICATION NUMBER: 60/350,493

PRIOR PILING DATE: 2001-11-13

PRIOR FILING DATE: 2001-11-13

WUMBER OF SEQ ID NOS: 34-11-13
                                                781 ATCCTAAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC
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Pred. No. 5.3e-304;
0; Mismatches 22;
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SEQ ID NO 5
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; ORGANISM: Macaca fascicularis
US-10-291-990-5
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Best Local Similarity 97.8%;
Matches 1001; Conservative
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Accordance   101;   Conservative   0;   Mismatches   22;   Indels   0;   Gaps   0;   Accordance   1;   Accodance   1;		RESULT 13 US-10-309-515-33 ; Sequence 33, Application US/1030;	; PUBLICANT OSCOJOURACE ; APPLICANT Bennett Kinrade, Mic. ; APPLICANT: Brodbeck, Robbin M.	APPLICANT: Waters, Stephen M. ; APPLICANT: Krause, James E. ; TITLE OF INVENTION: Melanin Conce ; FILE REFERENCE: NOW. 2020.	; CURKENT AFFLIATION NUMBER: 05/ ; CURRENT FILING DATE: 2002-12-0 ; PRIOR APPLICATION NUMBER: 60/28 ; PRIOR FILING DATE: 2001-04-19 ; DATOR DADE: COATON NUMBER: 10/12	PALOR FILING DATE: 2002-04-18 ; PRICR FILING DATE: 2002-04-18 ; NUMBER OF SEQ ID NOS: 60 ; SOFWARE: Patentin version 3.1 ; SEC TD NO 33	, 0,	Query Match  Query Match  Best Local Similarity 97.7%; P. Matches 999; Conservative 0;	9y 1 ATGAATCCATTTCATGCATCT	ΨΨ	Oy 1	Oy 181 OD 181	Qy 241	0y 301	0y 361	0y 421 0h 421	Qy 481	0 QY 541 G	Db 541 GTCGAGAGTTGTGCTTTTGAT Qy 601 TTGACGATAACAACTTTTTT	
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Db 601 TIGACAATAACAACTITCTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660  Qy 661 TTATGCTATACTTGGGAGATGTATCAACAAATAAGGATGCCAGATGCTGCAATCCCAGT 720  Db 661 TTATGCTATACTTTGGGAGATGTATCAAAATAAGGATGCCAGAATGCTAGAATGCCAGT 720	721 GTACCAAACAGAGAGTGATGATTGACAAAGATGGTGCTGCTGGTGCTAGTTT 78	781 ATCCTAAGTGCCCCTTATCATGTACAACTGGTGAACTTACAGTGGAACGCCC 781 ATCCTAAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGTGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGAACGGAACGGAACGGAACGGAACGGAACGGAACGCAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGCAACGAACGCACCCAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACAAC	Qy         841 ACACTGGCCTTCTADGGGTTATTACCTCTCCATCTCTCAGCTATGCCAGCAGC         900           Db         841 ACACTGGCCTTCTATGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGC         900	ATTAACCTTTTCTCTACATCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATCTTTTTCCAGAAACGTCTGCTCAAATCTTTCCAGAAACGTCTGCTCTGAAATCTACCTTTTTCTCTACCTTCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC	CAAAGAAGAGGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1	1021 TAG 1023	SULT 14		1	; IIILE OF INVENTION MORKEY and Canine Melanin Concentrating Hormone Receptors; FILE REPRENCE: NOI.2102; CURRENT APPLICATION NUMBER: US/10/291,990; CURRENT FILING DATE: 2002-11-12; CURRENT FILING DATE: 2002-11-12.	FRIOR RFILING DATE: 2007-11-13  NUMBER OF SEQ ID NOS: 34  SOFTWARE: Patentin Version 3.1	; SEU ID NO I ; LENGTH: 1023 ; TYPE: DNA ; ORGANISM: Macaca fascicularis ns.10-291-890-1	Query Match 96.2%; Score 984.6; DB 15; Length 1023; Best Local Similarity 97.7%; Pred. No. 5.6e-303; Matches 999; Conservative 0; Mismatches 24; Indels 0; Gaps 0;	OY 1 AIGAAICCAITICAIGCAICTIGTHGGAACACCTCTGCCGAACTITTAAACAAAICCTGG 60	OY 61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120	Qy 121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180	Oy 181 AGAICCAGGAAAAAAGACCCTGACATCTATATCTGCAACCTGGCGGCTGATTG 240

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	Query Match	100.0	100.0	100.0	100.0	100.0		100.0		100.0				8.66	8.66	99.8	99.8	96.6	96.4			96.2	9	96.1
	Score	1023	1023	1023	1023	1023	1023	1023	1023	1023	1023	1023	1023	1021.4	1021.4	1021.4	1021	ω	986.2	984.6	984.6	84.	m	983
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	1 Ferret MC	3 Human MCH	_					10 Dog MCH-2	9 G protein	9 cDNA isol	1 Human GPC		.9 Cat melan	4 Human G P	2 Cat melan	4 Human sec	13 Monkey MC		7 DNA encod	3 Nucleotid	2 Dog melan
Aad29677	Aad48421	Aad48423	Ade24771	Ade24745	Ade24772	Ade24755	Aad62477	Aad48420	Abk10849	Aaf93609	Adc12691	Abz36066	Ade24739	Aas4284	Ade24742	Aac03164	Aad62483	Aad62489	Aas42937	Aaf85373	Ade24752
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95.9	86.7	86.7	85.0	84.7	82.8	81.6	81.6	81.2	70.0	47.3	46.3	44.8	36.1	29.9	26.5	24.2	22.5	21.2	21.1	21.1	19.7
981.4	887	887	869.4	866.4	846.6	834.6	834.6	831	716	484.2	473.6	458.2	368.8	306.2	270.6	248	230.2	216.6	215.4	215.4	201.6
24	25	56	27	28	5	30	31	32	e e	34	35	36	37	38	39	40	41	42	43	44	4.5
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## ALIGNMENTS

AAA90097 standard; DNA; 1023 BP.

AAA90097;

G-protein coupled receptor; SLT, antiallergic, antirheumatic; antidiabetic; nootropic; neuroprotective; antiinflammatory; neuroleptic; hypotensive; nervous system disorder; hormonal disorder; schizophrenia; inflammatory diseases; cardiovascular disease; Alzheimer's disease; allergy; rheumatism; sodium intolerance; diabetes; hypertension; ds. G protein coupled receptor protein SLT, DNA encoding it and antibodies recognizing it, useful for treatment and diagnosis of e.g. neurological This invention relates to a G-protein coupled receptor protein, SLT of human origin. The nucleotide and protein sequences are given in the specification. The invention includes expression vector containing SLT encoding polynucleotide sequences, host cells transformed with the vectors, and methods for preparing SLT through the culturing of the transformants. Also included are anti-SLT antibodies, SLT ligands and Human G-protein coupled receptor SLT encoding DNA sequence. Shintani Y; Claim 5; Fig 1; 108pp; Japanese. 99JP-00125768. 18-FEB-2000; 2000WO-JP000927. (TAKE ) TAKEDA CHEM IND LID. (first entry) Watanabe T, Terao Y, WPI; 2000-543749/49. P-PSDB; AAB23540. WO200049046-A1. Homo sapiens. 19-FEB-1999; 06-MAY-1999; 02-JAN-2001 24-AUG-2000. diseases. 

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         antirheumatic, antidiabetic, nootropic, neuroprotective, antidiabetic, and hypotensive activity. The g protein coupled receptor protein SLT, the DNA encoding it and its antibodies can be used for the diagnosis and treatment of diseases with which SLT is associated, such as disorders of SLT expression. These include nervous system disorders, hormoral disorders, inflammatory diseases, and liver/gall bladder/panceas diseases (such as Alzheimer's disease, and liver/gall bladder/panceas diseases (such intolerance, diabetes and hypertension). The present sequence represents
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0
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exhibits antiallergic,
                                                                                                                                                                       Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;
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                                                                                                                                                                                                100.0%; Score 1023; DB 3;
100.0%; Pred. No. 1.8e-295;
ive 0; Mismatches 0;
their identification. SLT
                                                                                                                                             SLT DNA sequence of the invention
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Best Local Similarity 100.
Matches 1023; Conservative
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The present sequence encodes a human G-protein coupled receptor, designated HG67 or MCH-R2. HG67 is a melanin concentrating hormone receptor. Modulators of HG67 can be used to treat a patient, particularly to reduce weight, particularly in obesity, or to treat stress. These modulators can also be used to treat cancer, reduce pain, treat sexual dystunction or to produce weight gain. Bringing about weight loss can be used to reduce the likelihood of hypertension, diabetes, dyslipidemia, cardiovascular disease, gall stones, osteoarthritis or certain forms of
 006
                                                                                                                                                                                                                                                                                                                                                                                                     G-protein coupled receptor; HG67; MCH-R2; weight loss; obesity; stress; melanin concentrating hormone receptor; cancer; pain; sexual dysfunction; weight gain; hypertension; dyslipidemia; cardiovascular disease; gall stone; osteoarthritis; cancer; diabetes; anorexia; AIDS; wasting;
               ATTAACCCTTTTCTTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC
                                                                                                                     CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT
841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC
                                                                                                                                              caaagaagagagagaaggaaarcaacaarargggaaacacrcrgaaarcacarrr
                                                          901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC
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                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of human G-protein coupled receptor HG67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "G-protein coupled receptor HG67"
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1. .1023
/*tag= .a
/product= "G-protein
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2000US-0188977P.
2000US-0198029P.
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BANYU PHARM CO
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P-PSDB; AAB68428.
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13-MAR-2000;
18-APR-2000;
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cachexia;
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nervosa;

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The invention relates to a novel protein comprising a fully defined 340 amino acid sequence, or the sequence contenting one or more amino acid substitutions, deletions or insertions. The protein shows melanin concentrating hormone (MCH) receptor activity. It is a G protein coupled receptor that binds to MCH. The protein is used to find agents to treat obesity, cachexia, anorexia nervosa and hyperphagia. The present sequence encodes the protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                   61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG
                   CAAAGAAGAGCGACTGAGAAAGGAAATCAACAATATGGGAAAACACTCTGAAATCACACTTT
                                              CAAAGAAGAGCGACTGAGAAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AIGAAICCAFITCAIGCAFCTIGITGGAACACCTCTGCCGAACTTTAAACAAATCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New protein with melanin concentrating hormone receptor activity, finding antagonists for treating obesity and eating disorders.
                                                                                                                                                                                                                                                                               hormone receptor coding sequence
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                                                                                                                                                                                                                                                                                                         Human; melanin concentrating hormone; MCH; MCH receptor; G protein coupled receptor; obesity; cachexia; anorexia hyperphagia; anorectic; antianorectic; ss.
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Pred. No. 1.8e-295;
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100.0%; Pred. No. 1...
0; Mismatches
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Y;
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                                                                                                                                                                                        standard; cDNA; 1023
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                                                                                                                                                                                                                                                                                Human melanin concentrating
                                                                                                                                                                                                                                                  (first entry)
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Oda T, Saito
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(HELI-) HELIX RES INST.
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P-PSDB; AAM51567.
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cancers. Increasing weight can be useful in the treatment of anorexia, AIDS, wasting, cachexia and frail elderly patients, or those undergoing chemotherapy or radiation therapy
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Pred. No. 1.8e-295;
Mismatches 0;
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Best Local Similarity 100.0%; Pr
Matches 1023; Conservative 0;
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The sequence encodes a human G-protein coupled receptor (GPCR), hRUP27. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system; incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents.
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                                               G-protein coupled receptor, GPCR, hRUP27, agonist,
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Human cDNA encoding G-protein coupled receptor, hRUP27
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                                                                                                                                                                                Location/Qualifiers
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/*tag= a
/product= "hRUP27"
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990S-0171901P.
990S-0171902P.
20000S-0181749P.
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2000US-0242332P.
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10-APR-2000; 2000US-0196078P.
28-APR-2000; 2000US-0200419P.
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26-SEP-2000;
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AAS07954 standard; cDNA; 1023 BP

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                                  ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTAAACAAATCCTGG
                                                                                                          AATAAAGAGTTIGCTTATCAAACTGCCAGTGGGAGATACAGTCATCCTCCCTTCCATG
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The invention describes a method of screening for compounds or their salts that can change affinity of melanin-concentrating hormone (MCH) with its G protein-coupled orphan receptor protein, SLT. The screened MCH receptor agonists are useful as appetite-stimulating agents and its antagonist for preventing or treating obesity e.g. malignant mastocystosis, exogenous obesity and hyperinsulinar obesity, and also for treating sexual function disorders, overpowering intermittent pains, still borns, uterus rupture, premature birth and Prader-Willi syndrome. This sequence encodes the G protein-coupled orphan receptor protein, SLT
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concentrating hormone with its receptor to provide agonists as appetite-
stimulating agents and its antagonist for preventing or treating obesity,
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                                                                                                                G protein-coupled orphan; receptor; SLT; melanin-concentrating hormon MCH; appetite-stimulating agent; obesity; malignant mastocystosis; exogencus obesity; hyperinsulinar obesity; sexual function disorder; overpowering intermittent pain; still born; uterus rupture; premature birth; Prader-Willi syndrome; gene; ss.
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/product= "SLT"
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llarity 100.0%; Pred. No. 1.8e-295;
Conservative 0; Mismatches 0.
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                                                                                       G protein-coupled
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Human; TGR342; gene; ss; G-protein coupled receptor; GPCR; TGR;

BP.

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ABK86285 standard;

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Human TGR342 27-AUG-2002

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The invention relates to a G-protein coupled receptor polypeptide (GPCR), termed TGR, and its associated nucleic acid. The sequences of the invention are useful for identifying a compound that modulates signal transduction and for identifying a mammal having a TGR-associated is transduction and for identifying a mammal having a TGR-associated is transduction and for identifying a mammal having a TGR-associated is transduction and for identifying a mammal having a TGR-associated and include in diagnosis and transductions, hyperprolactinations such a renal failure, nephritis, the protection is proported, growth disorders, diabetes insipidus, hyperprolactinaemia and disturbances of thirst, sheep, temperature regulation, appetite, blood pressure or any other syndrome or disease associated with the hypothalamus. The sequences can be used in regulation of mutations associated with diseases resulting for the identification in particular cell types and for identification of modulators of GPCR signal transduction. This sequence represents cDNA cooling the human TGR342 polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated G-protein couple receptor polypeptide, termed TGR, for diagnosis and treatment of diseases such as renal failure, nephritis, hypothyroidism, diabetes insipidus, and disturbances of thirst and sleep.
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TGR-associated disorder; signal transduction; renal failure; nephritis; hypothyroidism; hypothoradism; retainitis pigmentosa; growth disorder; diabetes insipidus; hyperprolactinaemia; thirst disturbance; appetite; sleep disturbance; temperature regulation; blood pressure; hypothalamus;
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22-DEC-2000; 2000US-0257656P.
12-JAN-2001, 2001US-0251377P.
28-MAR-2001; 2001US-025954P.
29-MAR-2001; 2001US-0280696P.
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                                                                                                                                                                                                                                                                                  Melanin concentrating hormone type 2 receptor; MCH2R; hyperphagic; hypophagic; body weight; locomotor activity; stress; anxiety; sleep disorder; fatigue; circadian rhythm; energy metabolism; pain;
                                                                                                                                                                                                                                                 Human melanin concentrating hormone type 2 receptor (MCH2R) cDNA.
                                                                                                                            1.023
                                                                                                                                                                                                         (first entry)
                                                                                                                               CDNA;
                                                                                                                            AAD36796 standard;
                                                                                                                                                                                                         24-FEB-2003
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AAD3679

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The invention relates to a melanin concentrating hormone type I receptor (WCHIR) deficient mouse whose genome comprises an alteration in one or both MCHIR alleles, where the alteration substantially reduces expression of a functional MCHIR. The invention also relates to a method of measuring the affect of a compound on a MCHIR deficient mouse and measuring one or more phenotypes associated with MCHIR activity e.g. hyperphagic activity, body weight, locomotor activity. The methods and composition of the present invention are useful for screening of compounds that are further used as a research tool and for treating weight loss or weight gain, reducing pain, stress, anxiety, and treating weight loss or weight gain, reducing pain, stress, anxiety, and treating worder. Several dysfunction, diabetes, locomotor deficits, fatigue or sleep disorders. The present sequence is human melanin concentrating hormone type 2 receptor (MCH2R) CDNA used in a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCHIR deficient mouse with an alteration in one or both alleles, useful for screening of compounds as a research tool and for achieving useful effects for locomotor activity, stress, anxiety, fatigue, circadian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA
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                                                                                                                                /product= "MCH2R"
/note= "Melanin concentrating hormone type
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; Pred. No. 1.8e-295;
0; Mismatches 0;
cancer; sexual dysfunction; diabetes; human;
                                                                       Location/Qualifiers
1. .1023
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 31; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 1023; Conservative 0
                                                                                                                                                                                                                                                                                                         22-MAR-2001; 2001US-0278061P.
                                                                                                                                                                                                                                                                       19-MAR-2002; 2002WO-US008413
                                                                                                                                                                                                                                                                                                                                                (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                            2003-018901/01.
                                                                                                                                                                                                                                                                                                                                                                                       Qian S, Marsh DJ;
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                                          sapiens
                                                                                                                                                                                                                                03-OCT-2002
                                          Homo
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The invention relates to truncated melanin-concentrating hormone (MCH) analogue peptide active at melanin-concentrating hormone-2 receptor (MCH-2R), or its labelled derivative or salt, useful for increasing weight or appetite in a subject. The peptide is useful for screening for a compound able to bind MCH-2R. It is useful for increasing weight or appetite in a subject having an MCH-2R. It is useful for measuring the ability of a compound to decrease weight or appetite in a subject having MCH-2R. It is useful for measuring the ability of a screen for MCH agonists, to explore differences between MCH-1R and MCH-2R. The present sequence is human MCH-2R CDNA
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                                                                                                                                                                                                                              Novel truncated melanin-concentrating hormone analog peptide active at melanin-concentrating hormone-2 receptor, or its labeled derivative or salt, useful for increasing weight or appetite in a subject.
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Best Local Similarity 100.0%; Pred. No. 1.8e-295;
Matches 1023; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                           Example 1; Page 59; 30pp; English.
                                                                                                  31-MAY-2001; 2001US-0294806P.
                                                                                                                                                                                       WPI; 2003-201270/19.
                                                                                                                              (MERI ) MERCK & CO
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                                                                                       TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT
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                                                                       AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA
                                                                                                                                                        CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human melanin-concentrating hormone-2 receptor (MCH-2R) cDNA.
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/*tag= a
/product= "Human MCH-2R protein"
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This invention relates to novel truncated human melanin-concentrating receptor (MCH-1R). MCH has been localised to the meuronal cell bodies of the hypothalamus which are implicated in the control of food intake, including perikarya of the lateral hypothalamus and zona inertia. The primary mode of action of MCH is to promote feeding (orexigenic). The peptides of the invention, MCH-1R agonists, may have anti-HIV, anabolic or immunomoulator activities. The peptides may be useful for increasing weight/appetite in a subject having an MCH-IR. They may also be useful for measuring the ability of a compound to decrease weight/appetite in a subject having an MCH-IR. They may also be useful a subject having an MCH-IR. They may also be useful a subject having an MCH-IR. They may also be useful a subject having an MCH-IR. They may also be useful and the periods.
                                                                                                                                                                                                                                                                                                                                                                                                      subject to produce weight appetite increase, administering the compound, and measuring the change in weight or appetite of the subject. The peptides may therefore be useful for treating disorders accompanied by weight loss including anorexia, AIDS, wasting, cachexia and frail elderly diseases. The invention offers the advantages of ease of synthesis and/or increased solubility in physiological buffers. The present sequence is the DNA sequence encoding the human melanin-concentrating hormone (hMCH) type 2 receptor (MCH-2R) against which the peptides of the invention are specifically not targeted
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                                                                             New optionally substituted truncated human melanin-concentrating hormone (hMCH) peptides are hMCH-1 agonists, useful for increasing appetite/weight.
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Pred. No. 1.8e-295;
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                                                                                                                                                                Example 1; Page 20-21; 55pp; English.
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Matches 1023; Conservative 0:
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                                   2003-646040/61
                                                     P-PSDB; AAO27467
Sednarek MA;
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TCCTTTATCCTGGCATTGCCTGTCTGGGTCTTCGAAGGTCATCAAATTTAAAGACGGT
                                                         GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT
                                                                                                               TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT
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The invention relates to human G protein-coupled receptor (GPCR), HGPRRMY9 and its nucleic acid sequence. The invention is useful for preventing, treating, or ameliorating a medical condition related to the brain, lung, colon, testes, neural, gastrointestinal, pulmonary, or reproductive system. Detecting mutations in HGPRBMY9 bib actermining the level of expression of HGPRBMY9 is useful in diagnosing disease. HGPRBMY9 nucleic acid, polypeptide and agents that control the level of expression or activity of HGPRBMY9 may be useful in treating conditions such as cancer, Alzheimer's disease, asthma, and diabetes. The present sequence is human HGPRBMY9 cDNA
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                                                                                                                                                    New human G-protein coupled receptor and its encoding polynucleotide useful for treating and diagnosing conditions such as neurological disorders and disorders of the testes.
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                                                           Hawken DR,
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                                                           Ramanathan CS,
                                                                                                                                                                                                                                    Claim 1; Fig 1; Opp; English.
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P-PSDB; ABW00463.
HAWKEN D R.
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concentrating hormone with its receptor to provide agonists as appetite-
stimulating agents and its antagonist for preventing or treating obesity,
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The invention describes a method of screening for compounds or their salts that can change affinity of melanin-concentrating hormome (MCH) with its G protein-coupled orphan receptor protein, SLT. The screened MCH receptor agonists are useful as appetite-stimulating agents and its antagonist for preventing or treating obesity e.g. malignant mastocystosis, exceptones obesity and hyperinsulinar obesity, and also for treating sexual function disorders, overpowering intermittent pains, still borns, uterus rupture, premature birth and prader-willi syndrome. This sequence encodes the G protein-coupled orphan receptor protein, SLT
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Best Local Similarity 100.0%; Pred. No. 1.9e-295;
Matches 1023; Conservative 0; Mismatches 0;
2; Page 96-97; 112pp; Japanese.
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721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT
          4; Page 92-93; 279pp; English
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                                                                                                                                                                                                                                                                                               Human, G-protein coupled receptor, GPCR, mental disorder, schizophrenia, attention deficit disorder, anxiety, depression, bipolar disorder, ss; neurological disorder, Huntington's disease; dementia, obesity, anorexia, metabolic disorder, Parkinson's disease; Pourette's syndrome, thrombosis, type 2 diabetes; cardiovascular disorder, myocardial infarction, cancer, cardiomyopathy; atherosclerosis, human immunodeficiency virus; HIV; viral infection; immunostimulant; neuroleptic, nootropic; tranquiliser; antidepressant; anorectic, PCR primer; gene therapy.
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                                                                                       ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 966
ALCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAAACTTACAGATGGAAACAGCCC
                              ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC
                                                                     CICTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC
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03-MAR-2000; 2000US-018680P.
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Sequences AAS42806-AAS42926 represent cDNA molecules and PCR primers for CDNA molecules encoding human G-protein coupled receptor (GPCR) polypeptides. The protein and DNA sequences of the invention can be used to identify compounds which bind to GPCR polypeptides and in screening for compounds that modulate GPCR activity. By screening a human subject for the presence of mutations in GPCR DNA, a GPCR-related disorder or a genetic predisposition can be diagnosed. The sequences can also be used for treatment and prevention of mental disorders such as schizophrenia, attention deficit disorder, anxiety, depression, dementia and bipolar disorder, neurological disorders such as Huntington's disease, Parkinson's disease and Tourette's syndrome, metabolic disorders such as thrombosis, myocardial infarction, cardiovascular disorders such as viral infections caused by HIV and cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1965 BP; 547 A; 422 C; 402 G; 594 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 1023; Conservative
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GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG
Huntington's disease or Gilles de la Tourette's syndrome. AXOR21 polymucleotides and polypeptides are also useful for screening and structure based designing of antagonists, agonists and inhibitors of AXOR1. AXOR21 polymucleotides are useful for chromosome localisation studies, as diagnostic reagents for defecting mutetions in associated genes, and as valuable tools for tissue expression studies. AXOR21 polymucleotides and polypeptides are useful as vaccines
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                                                                                                                                 C; 222 G; 307 T; 0 U; 0 Other;
                                                                                                                                                                 Score 1021.4; DB 5
Pred, No. 5.6e-295;
); Mismatches 1;
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                                                                                                                                     Sequence 1023 BP; 264 A; 230
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Best Local Similarity 99.9%;
Matches 1022; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, AXOR21; G-protein coupled receptor; anorectic; antidiabetic; cytostatic; antidashmatic; antiparkinsonian; cardiant; hypertensive; osteopathic; antianginal; cerebroprotective; antiulcer; antiallergic; antimigraine; antiemetic; tranquiliser; antimanic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel G-protein coupled receptor polypeptide, AXOR21, useful for treat obesity, diabetes, eating disorders such as ancrexia and bulimia, hypertension, osteoporosis, angina pectoris and myocardial infarction.
     GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTGGTTTTT
                                                                                                                                                                                                                                                                        CAAAGAAGAGCGACTGAGAAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT
                                                      ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC
                                                                           ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACCC
                                                                                                                     ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC
                                                                                                                                                    ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; neurological disorder;
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99GB-00020046.
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24-AUG-1999;
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The invention relates to novel seven transmembrane domain receptors, designated 6549 or 58875. The 65499 and 58875 polypeptides can be expensed by standard recombinant methodology. The polypeptides can be expected to standard recombinant methodology. The polypeptides, encoding polymucleotides and modulators are useful for controlling G protein coupled receptor-related disorders, and as a novel diagnostic target and therapeutic agent in treatment and diagnosis of 65499 or 58875 mediated the related disorders such as callular proliferative and differentiative disorders (including cancer e.g., carcinoma, sarcoma), bone metabolism disorders (e.g., osteoporosis, rickets,), haematopoietic disorders (such as chronic myelogenous leukemia, acute promyeloid leukemia,), cardiovascular disorders (e.g., isohaemic heart disease, myozardial infarction, etc), endotholial cell disorder (e.g., portiasis, Grave's disease,), hormonal disorders (e.g., multiple sclerosis, Parkinson's immune disorders (including autoimmune diseases such as rheumatoid
                                                                  CAAAGAAGAGGGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
                                                                                                   1020
                               960
                                                                                                                                                                                                                                                                                                                                                                                                Human, seven transmembrane domain receptor; 65499; 58875; cytostatic; osteogratic, andipsoriatic, antichtyvoid; gene; ds neuroprotective; anniparkinsonian; antidiabetic; virucide; analgesic, antirheumatic; antiarthritic; anorectic; immunomodulator; gene therapy.
                  ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC
                                                                                    CAAAGAAGAGGGACTGAGAAAAGAAATCAACAATATGGGAAAACACTCTGAAATCACACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wover isolated 65499 or 58875 polypeptide, novel seven transmembrane domain receptors, useful as reagents or targets for treatment or diagnosis of rheumatoid arthritis, ischemic heart disease, Grave's disease, obesity.
                                                                                                                                                                                                                                                                                                                                                                 Human seven transmembrane receptor, 58875 protein coding sequence.
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                                                                                                                                                                                                                                                                            Human; seven transmembrane domain receptor; 65499; 58875; cytostatic; osteopathic; vasotropic; cardiant; antipsoriatic; antichyroid; gene; ds; neuroprotective; antiparkinsonian; antidiabetic; virucide; analgesic; antirheumatic; antiparkinsonian; anorectic; immunomodulator; gene therapy.
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/note= "the coding sequence (ABL41166) is specifically
                ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC
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                                                                                                                                                                                                                                                     seven transmembrane receptor, 58875 protein encoding DNA.
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Pred. No. 6.2e-295;
0; Mismatches 1; Indels 0;
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Matches 1022; Conservative
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qq	1048	ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC
δ	961	961 CAAAGAAGAGCGACTGAGAAAGAAATCAACAATATGGGAAACACTTT
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TITLE
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                                       Result
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1 (bases 1 to 1023)

Liu.Q., McDonald,T.P. and Howard,A.D.

Nucleic acid molecule encoding a melanin-concentrating hormone receptor 2 polypeptide
Patent: US 6593108-A 2 15-JUL-2003; score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Ното AF347063 BD097497 AB058850 AY078246 AF513989 BD141141 AR169786 BD274496 AX459698 AF399937 AX459695 AB060151 AC027643 AX230124 BD013164 BD141137 AX079686 AX657440 linear DNA ALIGNMENTS AR353776 1023 bp Sequence 2 from patent US 6593108. AR353776 1GI:33759828 SUMMARIES Length DB 231.00 24.00 22.20 14.2 14.2 13.2 3.3 Query W 80 W 10 Unknown Unknown COURNAL

Qy         961         CAAAGAAGAGGACGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT         1020           Db         961         CAAAGAAGAGGACTGAGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT         1020           Qy         1021         TAG         1023           Db         1021         TAG         1023	RESULT 2 AX148198 LOCUS LOCUS DEFINITION Sequence 39 from Patent W00136471.  AX148198 AX14819	Query Match   100.0%;   Score 1023;   DB 6;   Length 1023;   Best Local Similarity   100.0%;   Pred. No. 8.7e-274;   Matches 1023;   Conservative   0, Mismatches   0;   Indels   0;   Gaps   0;   O;   ATGAATCCATTTCATGCAACACACTCTGCCGAACTTTTAAACAAATCCTGG   0   O   1 ATGAATCCATTTGATGCATCTTGTTGAACACTCTTGCTGCGAACTTTTAAACAAATCCTGG   0   O   1 ATAAAGAGTTTGATCATCTTGTTGAACACTCTTGCTGGCGAACTTTTAAACAAATCCTGG   0   O   O   O   O   O   O   O   O   O	121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 121 ATTGGGATTATCTGTTCAACAGGGCTGGCTTGGCAACATCCTCATTGTATTCACTATAATA 121 ATTGGGATAACAGGGCTGGGTTGGCACATCCTCATTGTATTCACTATAATA 181 AGATCCAGGAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 181 AGATCCAGGAAAAAACAGTCCCTGACATTATCTGCAACCTGGCTGTGGCTGTTTG 181 AGATCCAGGAAAAAACAGTCCCTGACATTTTTTTTTTTT	1
FEATURES  Location/Qualifiers  source  1023	Qy         1 ATGAATCCATTTCATGCATCTTGTGGAACACCTTGCCGAACTTTTAAACAAATCCTGG 60           Db         -1 ATGAATCCATTTCATGCATCTTGTGGAACACTTTGCGGAACTTTTAAACAAATCCTGG 60           Qy         61 AATAAAGAGTTTGCTTATCAACTGCCAGTGTGGTAGATCACTCTCCCTTCCTG 120           Db         61 AATAAAGAGTTTGCTTATCAACTGCCAGTGTGGTAGATCACTCTCCCTTCCTGTG 120           Qy         121 ATTGGGATTATCTGTTCAACAGGCTGGTTGGCAACATCTCATTGTATCACTTAATA 180           Qy         121 ATTGGGATTATCTGTTCAACAGGCTGGTTGGCAACATCTCTATTGTATCACTATAATA 180           Qy         181 AGATCCAGGAAAAAAAACAGTCCTGGATTGGCAACATCTCATTGTATTCACTATAATA 240           Db         241 GTCCACAAAAAAAACAGTCCTTATTCACCAATGGCTGGTGGTTGGT	Oy         361 AGTGCCATCATGACTGTAATGAGTGGGACAGGTACTTTGCCCTCGACCATTTCGA 420           Db         361 AGTGCCATCATCACTGTAATGAGTGTGCACAGGTACTTTGCCCTCGTCCCACCATTTCGA 420           Cb         421 CTGACACGTTGGAGACAGGTACAAGCTTCGGATCAATTTGGGCAGCT 480           Cb         421 CTGACACGTTGGAGAACAGGTACAACATCGGATCAATTTGGGCAGCT 480           CC         421 CTGACACTTGGAGAACAGGTACAACATCCGGATCAATTTGGGCAGCT 480           CA         481 CCTTTAATCCTGGCACACCCTGCTGCTACTCGAAGGTCAACTAAAAGACGGT 540           CD         481 CCTTTAATCCTGGCATTGCTGGGTCTACTCGAAGGTCATTAAAAGACGGT 540	541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT  [	OY 721 GTACCARAACAGGGGTGATGAAGTTGAAGAGGTGCTGGTGCTGGTTGTTT 780  Db 721 GTACCARAACAGGGTGATGAAGTTCACAAGATGGTGCTGGTGCTGGTGTTT 780  721 GTACCARAACAGGGTGGTGAAGTTCACAAGATGGTGCTGGTGCTGGTGGTGTTT 780  OY 781 ATCCTGAGTGCTGCCCTTATCATGTGATACAACATGGTGAACTTACAGATGGAACAGACC 840  Db 781 ACCTGGCCTTCTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCC 840  OY 841 ACACTGGCCTTCTATGTGGTTATTACCTCTCTCTCTCTCT

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/db_xref="TG1:22290798"
/db_xref="REMTREMBL:CAD82887"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    1023
/note="unnamed protein product; human G-protein coupled
receptor (GPCR) TGR342, melanin-concentrating hormone

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/db_xref="taxon:9606"
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Gupte,J.S.
G-protein coupled receptors
Patent: WO 0242458-A 1 30-MAY-2002;
Tularik Inc. (US)
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	RESULT 4 BD003056 BD003056 BD003056 BD003056 BD003056 BD003056 ACCESSION BD003056 GT:18631017 KEYWORDS GT 201017186-A/1. SOURCE HOWO Sapiens (human) ORGANISM HOmo Sapiens (human) ORGANISM Extractal Eutheria; Primates; Craniata; Vertebrata; Euteleostomi; BEFERENCE (bases 1 to 1023) AUTHORS Watanabe,T., Teraco, S. and Arraya,Y. TITH: Novel G protein-coupled arcestor protein and DNA thereof	Patent: JP 2001017136-A 1 23-JAN-2001; TAKEDA GERMICAL INDUSTRIES LTD OS HUMO saptens (human) PN 23-JAN-2001 PF 128-2000 PF 12	дар З	Qy         1 ATGAALCCATTTCATGCATCTTGTAGAACACCTCTGCCGAACTTTTAACAAATCCTGG         60           Db         1 ATGAATCCATTTCATGCATCTTGTTGGAACTTTTAAACAAATCCTGG         60           Qy         61 AATAAAGAGTTGCTTATCAACAGTGCAGTGGTAGATACAGTCATCCTCCCTTCCATG         120           Db         61 AATAAAGAGTTGCTTATCAACAGCCAGTGTGGTAGATACATCCTTCCATG         120           Oy         121 ATTGGGATTACTGTTAACAAGGCTGGTGGGAACATCCTATTGATAATAA 180           Db         121 ATTGGGATTATCTGTTCAACAGGCTGGTTGGCAACATCCTCATTGATTAATAA 180           Qy         181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATAATTATG 240           LB         AGATCCAGGAAAAAAACAGTCCTGACATCTATATTCTGGCTGTTGGCTGATTTG 240           LB         AGATCCAGGAAAAAAACAGTCCTGACATCTATATTCTGCCAACTGGTTGATTTG 240           LB         AGATCCAGGAAAAAAACAGTCCTGACATCTATATCTGCCAACTGGTTGATTTG 240           LB         AGATCCAGGAAAAAAAACGTCCTGACATCTATATCTGCCAACTGGTTGATTTG 240           LB         AGATCCAGGAAAAAAAACGTCCTGACATCTATATTCTGCAACTGGTTGATTTG 240

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YAMANOUCHI PHARMACEUTICAL CO LID, HELIX RESEARCH INSTITUTE, TAKESHI KURAMA, SHUNICHIRO MATSUMOTO, JUN TAKASAKI, MITSUTKII MATSUMOTO, MASAZUMI KAMOHARA, TETSU SAITO, TAMAKI ODA, YOKO SAITO OS HOMO SADIENS (luuman) PN WO 0170975-A/1 PP 23-MAR-2001 WO 0DP 00P 8888 PI 27-SEP-2001 PR 24-MAR-2000 JP 00P 8888 PI TAKASHI KURAMA, SHUNICHIRO MATSUMOTO, JUN TAKASAKI, MITSUVKI PI MATSUMOTO PI TAKASHI KURAMA, SHUNICHIRO MATSUMOTO, JUN TAKASAKI, MITSUVKI PI TAKASHI KURAMA, SHUNICHIRO MATSUVAH, 705, CORTILISHI HORO SADIENS (MINIMAIN)	ATGRATICATITICATGGATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAATCCTGG 60	0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0

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and

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CSTGLVGNILLVFTIIRSRKKTVPDIYICNLAVADLVHIVGMPFLIHQMARGGEWVFG
GPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAA
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Molecular characterization of a novel melanin-concentrating hormon molecular characterization of a novel melanin-concentrating hormon receptor: Evidence of its expression in lateral hypothalamus Umpublished

Chaes 1 to 1023)

Kurama, T., Matsumoto, S. and Takasaki, J.

Direct Submission
Submitted (28-MAR-2001) Takeshi Kurama, Yamanouchi Pharmaceutical Submitted (28-MAR-2001) Takeshi Kurama, Yamanouchi Pharmaceutical Takukuba, Ibaraki 305-6855, Japan (8-mail:kurama@yamanouchi.co.jp, Tel:81-298-54-1636, Fax:81-298-52-5412)
                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG
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Soga,T., Saito,Y., Oda,T., Masuho,Y.
   cds.
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Kamohara,M., Saito,T., So
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                                                                                        ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
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Feighner, S.D., Tan, C.P., Fukami, T., Iwaasa, H., Hreniuk, D.L., Morin, N.R., Sadowski, S.J., Ito, M., Ito, M., Bansal, A., Ky, B., Figueroa, D.J., Jiang, Q., Austin, C.D., MacNeil, D.J., Ishihara, A., Ishihara, M., Kanatani, A., Van der Ploeg, L.H.T., Howard, A.D. and Liu, Q. Direct Submission.

Submitted (10.APR-2001) Metabolic Disorders, Merck & Co., Inc., 126 E. Lincoln Av., RY80Y-265, Rahway, NJ 07065, USA
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ilarity 100.0%; Pred. No. 8.7e-274;
Conservative 0; Mismatches 0;
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/tissue_type="brain"
/dev stage="fetus"
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1 (bases I to 1023)

2 (lases I to 1023)

Sailer, A.W., Sano, H., Zeng, Z., McDonald, T.P., Pan, J., Pong, S.-S., Feighner, S.D., Tan, C.P., Fukami, T., Iwaasa, H., Hreniuk, D.L., Morin, N.R., Sadowski, S.J., Ito, M., Ito, M., Bansal, A., Ky, B., Fiqueroa, D.J., Jiang, Q., Austin, C.P., MacNeil, D.J., Ishihara, A., Inara, M., Kanatani, A., Van der Ploeg, L.H.T., Howard, A.D. and Liu, Q. Identification and characterization of a second melanin-concentrating hormone receptor, MCH-2R

Proc. Natl. Acad. Sci. U.S.A. 98 (13), 7564-7569 (2001)
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           AGIGCCAICAIGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA
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Sailer,A.W., Sano,H., Zeng,Z., McDonald,T.P.,
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E Sogai, T. and Yamamoto, J.

S Isogai, T. and Yamamoto, J.

E Isogai, T. and Yamamoto, J.

Direct Submission

Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

(E mailigenomicsephrico, jp, Telia 438-52-3965)

NEDO human CDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); CDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.

[location/Qualifiers
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Novel g protein-coupled receptors
Patent: WO 0162797-A 57 30-AUG-2001,
PHARMACIA & UPJOHN COMPANY (US)
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/db_xref="taxon:9606"
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Duckworth,D.M., Hill,J.S., Muir,A.I. and :
Axor21, a g-protein coupled receptor
Patent: WO 0107606-A I 01-FEB-2001,
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Location/Qualifiers
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    1023
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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/note="cloning vector: pME18SFL3'
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                                                  AGATCCAGGAAAAAAACAGTCCCTGACATCTATACCTGCAACCTGGCTGTGGCTGATTTG
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butherla, Primates, Catarrhini, Hominidae, Homo.
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65499 and 58875, novel seven-transmembrane receptors and uses
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Pred. No. 2.4e-273;
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Millennium Pharmaceuticals, Inc. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 6 from Patent W00228901.
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Db 481 TCCTTTATCCTGGCATTGCCTGTCTACTCAAAGGTCATCAAATTTAAAGACGGT 540  Qy 541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCTGACGATGTACTCTGGTATACACTTTAT 600  bb 541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTTATT 600  co		PESULT 15  AX459695 LOCUS DETRITION Sequence 3 from Patent W00228901. AX459695 AX459696 AX459695 AX459695 AX459695 AX459695 AX459695 AX459695 AX459696 AX459695 AX459696 AX4566	1.1LCYTWBAYQONKDARCCNPSYPKORYMKLTKAYLVIVVYFILSAAPYHYIQLYNDLQ MEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFOKRLPQIQRRATEKEINNMGN
EURATYOCA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 1023)  AUTHORS Wang, S., Behan, J., O'Neill, K., Weig, B., Fried, S., Laz, T., Bayne, M.,  Gustafson, E. and Hawes, B. E.  Identification and pharmacological characterization of a novel  Human melanin-concentrating hormone receptor, mch-r2  MEDLINE J143976  MEDLINE J1459838  L1459838  L1459838  AUTHORS Wang, S., Behan, J., Fried, S., Hawes, B. and Laz, T.  TITLE Direct Submission  JOURNAL Direct Submission  JOURNAL Submitted (12-JUL-201) Human Genomics/CNS, Schering-Plough Res  Inst., 2015 Galloping Hill Rd, Kenllworth, NJ 07033, USA  FRATURES  L. 1023  AUTHORS Source   Authom Sapiens"    Mol Lype-"MRMP   Authom Sapiens"	DS	Duery Match  99.8%; Score 1021.4; DB 9; Length 1023;  Best Local Similarity 99.3%; Pred. No. 2.4e-273;  ATGAATCCATTCATGCATCTGTAGGAACACCTCTGCGAACTTTTAAACAATCCTGG  ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCGGAACTTTTAAACAATCCTGG  ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCGGAACTTTTAAACAATCCTGG  ATGAATCCATTTCATACAACTGCCAGTGTGGTAGATACAGTCTCTCGTG  61 AATAAGGATTTACTTATACAACTGCCAGTGTGGTAGATACAGTCTCCTTGTTG  121 ATTGGGATTATCTGTTCAACAGGGCTGGTGGGTAGATACAGTCTCCTTCCT	OY 481 TCCTTATCTGGCATTGCCTGTCTGGTCTACTCGAGGTCATCATGAATTTAAAGAGGT 540

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Pred. No. 2.4e-273;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                      Patent No. 6593108

Patent No. 6593108

Patent No. 6593108

GENERAL INFORMATION

APPLICANT: Liu, Qingyun

APPLICANT: Howard, Andrew D.

APPLICANT: Howard, Andrew D.

APPLICANT: Wassa, Hisashi

APPLICANT: Sano, Hideki

TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR
FILE BEFERROE: 205794

CURRENT APPLICATION NUMBER: US/09/712,368

CURRENT FILING DATE: 2000-11-14

PRIOR APPLICATION NUMBER: 60/165,871

PRIOR APPLICATION NUMBER: 60/168,977

PRIOR APPLICATION NUMBER: 60/188,977

PRIOR PILING DATE: 2000-03-13

PRIOR PILING DATE: 2000-03-13

PRIOR PILING DATE: 2000-04-18

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastERQ for Windows Version 4.0
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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Pred. No. 3.8e-59;
0; Mismatches 1;
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APPLICANT: McDonald, Terrence P.
APPLICANT: McDonald, Terrence P.
APPLICANT: Howasa, Hisashi
APPLICANT: Iwasa, Hisashi
APPLICANT: Sano, Hideshi
APPLICANT: Sano, Hideshi
APPLICANT: Sano, Hideshi
APPLICANT: Osno, Hideshi
FILE REFERENCE: 20579Y
CURENT APPLICANTON NUMBER: US/09/712,368
CURRENT APPLICANTON NUMBER: 60/165,871
PRIOR FILING DATE: 1999-11-16
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-03-13
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 22
SEQ ID NOS: 22
SEQ ID NOS 4
SEQ ID NO 4
LENGTH: 925
PRIOR APPLICATION NUMBER: 60/198,029
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 925
LENGTH: 925
TYPE: DNA
ORGANISM: Human
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NAME/KEY: misc feature

LOCATION: (1)...(925)

CTHER INFORMATION: n = A,T,C or G
US-09-712-368-3
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Patent No. 6593108
GENERAL INFORMATION:
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Best Local Similarity 99.5%;
Matches 216; Conservative
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Best Local Similarity 99.5%;
Matches 216; Conservative (
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APPLICANT: Iwassa, Hissshi
APPLICANT: Sano, Hideshi
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 20579Y
CURRENT FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: 60/165,871
PRIOR PLING DATE: 1999-11-16
PRIOR PREDICATION NUMBER: 60/165,871
PRIOR PLILNG DATE: 2000-31-16
PRIOR PLILNG DATE: 2000-03-13
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Length 925;
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LOCATION: (1)...(925)
OTHER INFORMATION: n = A,T,C or G
OTHER INFORMATION: Antisense sequence of Sequence ID. No.
Patent No. 6593108
                              1; Indels
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Db 564 ACGCCAGGCTCATTCCCTTCCCAGGGGGTGCTGGGCATCCGCCTGCCAAACC 623  Oy 572 CTGACGATGTACTTTATTTGACGATAACAACTTTTTTTCCCTCTAC 631  Db 624 CGGACACTCACTTTACTGGTTCACTTTTTTTTTT	Db 789 GCACGGCCATCTGTCTGTTTTTTTGTGTGCCACCTCTATTTGTGTGCCGCACCTCTATTTTTTTT	478-601-3 ence 3, Application US/0947 ent No. 6221616 ERAL INPORMATION: LICANT: Salon, John A. LICANT: Laz, Thomas M. LICANT: Baz, Thomas M. LICANT: Nagorny, Raisas LICANT: Nagorny, Raisas LICANT: Wilson, Amy E. LICANT: Wilson, Amy E. LICANT: Wilson, Amy E. LICANT: WISON, Amy E. LICANT: LI	Query Match         14.2%; Score 144.8; DB 3; Length 1214;           Best Local Similarity         50.8%; Pred. No. 2.5e-36;           Matches 468; Conservative         0; Mismatches 427; Indels 27; Gaps 4;           Qy         104 TCATCCTCCTTCATGATTGGGATTATCTGTTCAACAGGCTGGTTGGAACTCCTCA           bb         144 TCATTATGCTTCCTGTTCATGATTGGTTCACAGGAAACTCCACGG           203         164 TTGTATTATATATAAGATCCAGGAAAAAAAAACACTCCTGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCCTCAGGAAACTCTCTAGTTCTTATTC 211           Db         204 TCATCTTTGTTGTGTGAAAGAACTCCACATAGTTGGAAACGTCCCCGAACTTCTTATTC 271           c
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Pred. No. 2.5e-36;
0; Mismatches 427;
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                                                                                     TYPE: DNA; CACANISM: Rattus norvegicus US-09-478-602-3
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APPLICANT: Laz, Thomas M.
APPLICANT: Laz, Thomas M.
APPLICANT: Nagorry, Raisa
APPLICANT: Wilson, Amy E.
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Horm;
TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
FILE REPERENCE: 574534\JPW
CURRENT APPLICATION NUMBER: US/09/478,602
CURRENT FILING DATE: 2000-01-06
EARLIER APPLICATION NUMBER: 09/224,426
EARLIER FILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTI VET: 2.1
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Pred. No. 1.1e-31;
0; Mismatches 396;
                                                                                                                                                                 RESULT 8
US-09-170-496D-51
Sequence 51, Application US/09170496D
Setent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Liaw, Chen W.
ITLE OF INVENTION: No. 655539-Endogenous, C.
TITLE OF INVENTION: No. 655539-Endogenous, C.
TITLE OF INVENTION: No. 655339-Endogenous, C.
TENGREN FILING DATE: 1998-10-13
SEQ ID NO 51
TENGRE: 1209
TUDE: NAN.
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Best Local Similarity 50.1%;
Matches 413; Conservative
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COGANISM: Homo sapiens
US-09-170-496D-51
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Pred. No. 9.7e-32;
                                                                                               APPLICANT: SATHE, GANESH
APPLICANT: SATHE, GANESH
APPLICANT: ELLIS, CATHERINE
APPLICANT: HALSEY, WENDY
TYPLE OF INVENTION: 11cby Genomic Sequence
TITLE OF INVENTION: 11cby Genomic Sequence
CURRENT APPLICATION NUMBER: US/09/218,467B
CURRENT FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 6
                                                                     Sequence 6, Application US/09218467B Patent No. 6362326
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ORGANISM: HOMO SAPIENS
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Best Local Similarity
Matches 413; Conserv
                                                    .09-218-467B-6
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APPLICANT: Laz, Thomas M .
APPLICANT: Laz, Thomas M .
APPLICANT: Magorny, Amisa
APPLICANT: Wilson, Amy E.
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
FILE REFERENCE: 57453/JFW/JHB
CURRENT APPLICATION NUMBER: US/09/224,426
CURRENT FILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0 - beta
SEQ ID NO 1
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APPLICANT: Chalmers, Derek T.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
SOFTWARE: PATENTIN VOS: 294
SOFTWARE: PATENTIN Version 3.1
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US-09-170-496D-191
; Sequence 191, Application US/09170496D
; Patent No. 6555339
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APPLICANT: Salon, John A.
APPLICANT: Bas, Thomas M.
APPLICANT: Magorny, Raisa
APPLICANT: Milson, Amy E.
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
FILE REPERENCE: 574539\John UMBER: US/09/478,602
CURRENT APPLICATION NUMBER: US/09/478,602
EARLIER APPLICATION NUMBER: 09/24,426
EARLIER FILING DATE: 1998-12-31
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    GAAGTTCCGGAAGCCCTCTGTGGCCACCCTGGTGATCTGCCTCCTGTGGGCCCTCTCCTT 722
                                                                                                                                                     723 carcaccarcaccicrererererarectagacricaricectreceaggagidener
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                                                                          TATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTTAAAGACGGTGTTGA
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APPLICANT: Salon, John A.

APPLICANT: Nagorny, Thomas M.

APPLICANT: Nagorny, Raisa

APPLICANT: Nagorny, Raisa

APPLICANT: Wilson, Amy E.

TITLE OF INVENTION: Braceding A Human Melanin Concentrating Hormone

TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof

TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof

CURRENT APPLICATION NUMBER: US/09/478,601

CURRENT FILING DATE: 2000-01-06

EARLIER APPLICATION NUMBER: 09/224,426

EARLIER FILING DATE: 1998-12-31

NUMBER OF SEQ ID NOS: 15
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Pred. No. 1.1e-31;
0; Mismatches 396;
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Matches 413; Conservative
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ORGANISM: Homo sapiens
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Pred. No. 1.2e-31;
0; Mismatches 396; Indels
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                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,809
FILING DATE: 13-JUN-1997
CLASSIFICATION: 3-56
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/357,675
FILING DATE: 15-DEC-1995
APPLICATION NUMBER: US/08/357,675
FILING DATE: 16-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Preseria, Paul F
REGISTRATION NUMBER: 23,031
REGISTRATION NUMBER: 23,031
REGISTRATION NUMBER: 23,031
REGISTRATION NUMBER: 23,031
TELEPHONE: 60-1407-0700
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al Similarity 50.1%;
413; Conservative
                                                                                                                                                                                 3: Diskette
IBM Compatible
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            610-407-0701
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & F
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                  ZIP: 19482-0980
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                          COMPUTER: IBM Com
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                                                                                             Gaps
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                                                 DB 3; Length 1269;
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                                         Score 130.4; DB 3; Length :
Pred. No. 1.1e-31;
0; Mismatches 396; Indels
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US-06-602-809-1
US-06-602-809-1
Sequence 1, Application US/08602809
Patent No. 6008012
GENERAL INFORMATION:
APPLICANT: BERGSWA, DERK
APPLICANT: BILIS, CATHERINE
TITLE OF INVENTION: HUMAN SOMATOSTATIN-LIKE R
TITLE OF INVENTION: ECEPTOR
UMBER OF SEQUENCES: 3
                                              12.7%;
50.1%;
                                                                                             Matches 413; Conservative
                                                                       Similarity
    US-09-478-602-1
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ADDRESSEE: Intellectual Proper
STREET: P. O. Box 1539-UW2220
STREET: F. O. Box 1539-UW2220
STATE: Pennsylvania
COUNTRY: USA
                                                                       CTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCT
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bergsma, Derk J
APPLICANT: Blis, Catherine E
TITLE OF INVENTION: Human Somatostatin Receptor
NUMBER OF SECUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 130.4;
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APPLICATION NUMBER: PCT/US95/16472
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NAME: SULTON, Jeffrey A
REGISTRATION UNDRER: 34,028
REFERENCE/DOCKET UNDRER:
FELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
TELEPAK: 610 270 5024
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSPY di
COMPUTER: IBM PC COMPOPER: PC-FLOSPEATING SYSTEM: PC-FLOSPEATING SYSTEM: PC-FLOSPEATING SYSTEM: PC-FLOSPEATING SYSTEM: PC-FLOSPEATING STATEM: P
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CLASSIFICATION:
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d. No. 1.2e-31;
Mismatches 396;
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Patent No. 603872
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BELIS, CATHERINE
TITLE OF INVENTION: NOVEL HUMAN 11CB SPLICE
TITLE OF INVENTION: ARIANT
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                                                        Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & 1
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                                                                                                      CURRENT APPLICATION: DOS SUPERIOR 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/984,288 FILING DATE: 03-DEC-1997 CLASSIFICATION:
                                                                                                                                                                                                                                                                        RRICK APPLICATION DATA:
APPLICATION NUMBER: 60/032,763
FILING DATE: 11-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: PRESTITA, PAUL F
REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                             REPERENCE/DOCKET NUMBER: 23,031
REPERENCE/DOCKET NUMBER: P505:
TELECOMMINICATION INFORMATION:
TELEPHONE: 610-407-0701
TELEPAX: 610-407-0701
TELEPAX: 84616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 846169
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1385 base pairs TYPE: nucleic acid STRANDEDNESS: single
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Best Local Similarity 50.1%;
Matches 413; Conservative
                                                                               OMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
VALLEY FORGE
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Search completed: May 17, 2004, 22:41:55 Job time : 187 secs

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ISM Homo saptens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 730)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

AL Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Berhesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILL at:
AQ747249 HS_5537_A
AQ311725 RPGT11-10
AQ11872 Pan trog1
AQ1805629 HS_3226_A
BQ953496 AGENCOURT
CE516999 tigT-GSS-
CF147812 AGENCOURT
AQ49253 HS_5123_A
CF147812 AGENCOURT
BX346496 BX346496
BX37646 BX367456
BIT57656 BX374433
BMR0549 AGENCOURT
BX32558 BX367856
BIT57659 G030257991
BIT757659 G030257991
BIT757649 BX376496
BX3250008 BX326588
BX326588 BX367890
BX326589 AGENCOURT
BX32659 BX326598
BX326140 AL921401
BX44157 BX24691
BX403413 BX403473
CC252714 AGENCOURT
CC187682 CH264-008
AK038389 Mus muscu
BX144173 DAM10. rer
F07228 HSC1ZF101 n
CB054665 NISC_gm05
AY40033 Pan trog1
AY400333 Pan trog1
CF147825 AGENCOURT
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CF996790
CK239769
BG329444
AY400676
AY400988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                         AQ492353
CCF147812
BX367456
BX77659
B1757659
B1757659
BX326588
BX326588
BX326588
BX326588
BX326588
BX350008
BX350008
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AY400332
BX403468
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AK038389
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513
1006
1006
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83672889
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81.4
80.8
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77.8
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77.4
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772.6
722.4
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CF147811
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BC038441 Homo sapi
B1914562 603179505
BX279838 BX279838
                                                                                                                       May 17, 2004, 16:04:17 ; Search time 3085 Seconds (without alignments) 9902.435 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                  Description
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                    version 5.1.6
- 2004 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
                                                                                        OM nucleic - nucleic search, using sw model
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BC038441
BI914562
BX279838
                                                                                                                                                                                                                                                                  IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                    GenCore
Copyright (c) 1993
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em gss rbhg: *
em gss vrl: *
gb gss: *
gb gss: *
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57.7
50.4
42.8
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Total number of Minimum DB seq Maximum DB seq

Database

Searched:

Perfect score:

on:

Sequence:

Scoring table:

601114162 AGENCOURT

Mus muscu Mus muscu

602429002

EST 25-JUL-2003

699.8 590 515.8

Score

Result 80.

```
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINI)
DNA Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov
Contact: nisc mgc@ndpi.nih.gov
Contact: nisc mgc@ndpi.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesieldy,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., (Mann,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho.S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,O.L., Mastello,C., Maskerije, Wastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop, S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                             BC038441 2372 bp mRNA linear HTC 04-MAR-2003
Homo sapiens, Similar to G protein-coupled receptor slt, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 62 Row:n Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14210483 This clone has the following problem: retained intron.

1. .2372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ATTGGGATTATCTGTTCAACAGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2372)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (04-CCT-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCTTCCATG
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/clone lib="NIH MGC_121"
/lab host="DH10B"
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688 ITAIGCIAIACTIGGGAGAIGIATICACAGAAIAAGGAIGCCA
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Pred. No. 2.1e-136;
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/mol type="mRNA"
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/db_xref="taxon:9606"
/clone="IMAGE:5243616"
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100.0%; Pre/
0; P
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                                                                                                                                                                                                                                      MAGE:5243616, mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg, R
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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llarity 99.7%; Pred. No. 6.9e-164;
Conservative 0; Mismatches 2; 1
                                                                                                                                                                       /organism="Homo sapiens"

mol_type="mRNN"

/db_xref="texon:9606"

/clone="TMAGE:6971912"

/tissue_type="mixed"
                                             07
          http://image.llnl.gov
Plate: IRB102 row: c column: 0'
High quality sequence stop: 667.
Location/Qualifiers
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Matches 701;
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sapiens cDNA clone IMAGE:5243616 5',
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
Plate: LLAMIGH row: j column: 01
High quality sequence stop: 660.
Location/Qualifiers
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: EcorV (destroyed); RNA source anonymous pool of stetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA
                                                                                       AGATCCAGGAAAAAAACGGTCCCTGACCATCTATATCTGCAACCTGGCGTGGCTGATTTG
                                                                                                                                               GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG
                                                                                                                                                                       GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGAAGAGGGGAGGGGTG
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                                                               <u> AGATCCAGGAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG</u>
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/db_xref="taxon:9606"
/clone="IMAGE:5243616"
/lab_host="DH10B"
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603179505F1 NIH_MGC_121 Homo
MRNA sequence.
B1914562.
B1914562.1 GI:16198951
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Homo sapiens
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0.7-3.5 kb. Library is normalized and enriched for
Mill.length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."
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1 (bases 1 to 507)
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schheider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                       190 ATTGGGATTATCTGTTCAACAGGCCTGGTTGGCAACATCCTCATTGTATTCACTATAATA
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RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Peld 580, D-69120 Heidelberg, Germany
RZPD, IMAGP9990111614.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
                                                                                                                                                                          .;
Έ
                                                                                                                                 Length 960;
                                                                                                                            Score 515.8; DB 12; Length
Pred. No. 6.4e-118;
0; Mismatches 27; Indels
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BX279838.1 GI:28612214
                                                                                                                              Query Match
Best Local Similarity 94.8%;
Matches 545; Conservative
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BX279838
                                                                                         ORIGIN
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AQ747249.1 GI:5534407
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                                                                                                                         Homo sapiens
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Matches 21
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      ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                         ORGANISM
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /douglib="Nature" // (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1) | (100 | 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTGGGATTATCTGTTCAACAGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGATCCAGGAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGALCCAGGAAAAAACAGLCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GICCACATAGTIGGAAIGCCTTITCTTAITCACCAAIGGGCCCGAGGGGGAGAGIGGGIG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            grecacaragriggaarecerrirerrarreaceaaregeeceaagggagagagggig 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITGGGGGGCCTCTCTGCACCATCATCACCTGCATACTTGTAACCAATTTGCCTGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 489
                                                                                                                                                                                                                                         This clone is available royalty-free from RZPD; contact RZPD (clonesrzpd.de) for further information. Seg primer: M13u, Primer sequence: CGTTGTAAAACGACGGCCAGT. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITCGGGGGCCTCTCTGCACCATCATCCTGGATACTTGTAACCATTTGCCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Human UnigeneSet - RZPD3 (RZPDILB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl.cgi/response?libno=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Fax: +49 30 32639 101
www:rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/b_xref="taxon:9606"
/clone="!MAGp998J0111614 ; IMAGE:5243616"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 438; DB 13;
; Pred. No. 1.6e-98;
0; Mismatches 0;
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ilarity 100.0%; Pr
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGACACGTTGGAGACA 507
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Best Local Si
Matches 438
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AQ747249/c
LOCUS
DEFINITION
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GSS 19-JUL-1999

AQ747249

HS 5537 Al D09 T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1113 Col=17 Row=G, genomic survey sequence.

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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Voctor DA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
AQ311725/c 602 bp DNA linear GSS 04-MAY-1999
LOCUS AQ311725
DEFINITION RPCIll-100N2.TV RPCI-11 Homo sapiens genomic clone RPCI-11-100N2,
                                                                                                                                                                                and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 925).
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    474 regrecacaractregaarecerriterratreaceaareeeceaageeaageage
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                                                                                                                                                                                                                                              Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 TAAGATCCAGGAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATT
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0
                                                                                                                                                                                                                                          scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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99.5%; Pred. No. 6.7e-43;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=1113 Col=17 Row=G"
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Location/Qualifiers
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Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
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R.Site 1
R.Site 2
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                                                                                      Homo sapiens (human)

Homo sapiens (human)

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Eutaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 602)

Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,

Barry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.

Use of human BAC End Sequences for Sequence-Ready Map Building

Longublished (1998)

Contact: Shaying Zhao, William Nierman, Mark Adams

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Enkaryotic Genomics

The Institute for Genomic Research

712 Medical Center Dr., Rockville, MD 20850

Fax: 301 838 0200

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Pan troglodytes DNA, clone: PTB-127E10.R, genomic survey sequence.
AG118972
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/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
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100.0%; Pred. No. 2.5e-39;
ive 0; Mismatches 0;
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/db_xref="GDB:7538329"
/db_xref="taxon:9606"
/clone="RPCI-11-100N2"
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1. .602
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  genomic survey sequence.
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                        AQ311725
AQ311725.1 GI:4043474
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AG118972
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GSS. Pan troglodytes Pan troglodytes Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Fujiyama, A., Hatfori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Totoki, Y., Watanabe, H. and Sakaki, Y. Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submitssion

Direct Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKBN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@Scritken.go.jp), URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library FTB This BAC end clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 04-NOV-1998
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Adams, M.D. and
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
(bases 1 to 519)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. an
Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 CATCCAGATCAATTTGGGCCTTTGGGCAGCTTCCTTTATCCTGGCATTGCCTGTCTGGGT
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HS_3226_A1_H07_T7_CIT_Approved Human Genomic Sperm Library D Fapiens genomic clone Plate=3226 Col=13 Row=0, genomic survey
Fuliyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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Pred. No. 2.9e-38;
0; Mismatches 2;
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/organism="Pan troglodytes"
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/db_xref="taxon:9598"
/clone="PTB-127E10.R"
/sex="male"
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                                                                                Unpublished
2 (bases 1 to 714)
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181 AGAT 184
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NIH-MGC http://mgc.noi.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="CIT Approved Human Genomic Sperm Library D" /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH108"
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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              connectors: A sequence approach to mapping and
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Sequence-tagged connectors: A sequence approach to mapp. scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                          High Throughput Sequencing Center University of Washington Vol Queen Anne Avenue North, Seattle, WA 98109, USA 401 Queen Anne Avenue North, Seattle, WA 98109, USA Fax: (206) 616-3887
Email: jwallac@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 195.4; DB 28; Length
Pred. No. 6.2e-38;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/db_xref="taxon:9606"
/dbone="plate=3226 Col=13 Row=O"
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                                                                                                             Contact: Mahairas GG, Wallace JC,
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llarity 97.1%;
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653 bp DNA linear GSS 28-SEP-2003 tigr-gss-dog-17000327417623 Dog Library Canis familiaris genomic, genomic survey sequence.
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0208
Pax: 301-838-0208
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Kirkness B.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
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                    column: 19
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                                                                                                            /mol_type="mRNA"
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http://image.llnl.gov
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Homo sapiens (human)

Homo sapiens

Homo sapiens

Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases 1 to 764)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 RmloA07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: GPCR Consortium
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/clone="lib="Dog Library"
peripheral blood"
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D; Mismatches 24;
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ekirknes@tigr.org
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larity 87.0%;
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/clone_lib="NIH_MGC_145"
/clone_lib="NIH_MGC_145"
/clone_lebercor: pcDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR consortium. Cloning sites vary by clone and include the following: 5' EcoRvXmil/Khof-3', 5'-EcoRvXmil/Noc1-3', EcoRv (TA cloned, non-directional). For information about which gene each clones represented please visit our anonymous ftp site at ftp://image.libi.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NIH_MGC Library."
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1 (bases 1 to 429)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman T.
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Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S.,
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

El (Dases 1 to 723)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Orpublished (1959)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg: 31 Rah.0A07 Bethesda, MD 20892

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Tissue Procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium
Context: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Gueen Anne Avenue North, Seattle, WA 98109, USA
701 Tel: (206) 616-387
701 Email: Jwallace@u washington.edu
701 Library availability, please contact Pieter de Jong
701 Clones are derived from the human BAC library RPCI-11. For BAC
701 Library availability, please contact Pieter de Jong
701 Clones are derived from Library Avenue (http://bacpac.med.buffalo.edu/ordering_bac.htm)
702 from Resear h Genetics (info@resgen.com). BAC end Web Server:
703 Plate: 699 row: I column: 8
704 Parimer: 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib-"RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 25-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TICACCAAIGGGCCGAGNNGGGAGAGAGAGAGTGTTTGGGGGGCCTCTTGTGCACCATCATCA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 CATCCCTGGATACTTGTAACCAATTTGCCTGTAGTGCCATCATGACTGTAATGAGTGTGG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 CATCCCTGGATACTTGTAACCAATTTGCCTGTAGTGCCATCATGACTGTAATGAGTGTGG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCACCAATGGGCCCGAGGGGGAGAGTGGTGTTTGGGGGGGCCTCTCTGCACCATCATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%; Score 120.2; DB 28; Length 429; llarity 96.1%; Pred. No. 3.7e-19; Conservative 0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF147812
AGENCOURT 14740188 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:6971911 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol type="genomic DNA"
/db xref="taxon:9606"
/clone="plate=699 Col=8 Row=I"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 429.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                Class: BAC ends
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122; Conserv
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Best Local S
Matches 122
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VERSION
KEYWORDS
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AUTHORS
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COMMENT
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CF147812
    PUBMED
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                        COMMENT
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/mol_trye="mRNR"
/db xref="mRNR"
/db xref="mRNR"
/clone="IMAGE:6971911"
/tissue type="mixed"
/lab host="mH MGC-145"
/clone_lib="mH MGC-145"
/note="Vector: pcDNR3.1; Site 1: varies by clone; Site_2:
/note="Vector: pcDNR3.1; Site 1: varies by clone; Site_2:
/note="Vector: pcDNR3.1; Site 1: varies by clone; Orner of the GPCR Consortium. Cloning sites vary by pcDNR3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5' ECORV.Xmn1/Not1-3', ECORV (TA cloned, non-directional).
For information about which gene each clones represents, please visit our annonymous ftp site at presents, please visit our annonymous ftp site at a Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 GGAGACCATGTGCACCTCATCACGGCCATGGATGCCAATAGTCAGTTCACCAGCACCTA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGACTGAC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460
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Homo sapiens
Homo sapiens
Extravora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 988)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: IRBIO2 row: c column: 06
High quality sequence stop: 723.
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Pred. No. 9.7e-16;
0; Mismatches 184; Indels
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BX346496
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/organism="Homo sapiens"
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D Homo sapiens
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                                                                                                                             Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BRail: sequenceope.ons.fr, www.genoscope.ons.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10650.f For
http://www.genoscope.ons.fr/
cgi-bin/cluster.cgi?seq=CS0AQ004ZH10_A0368_l&cluster=10650.f.
cgi-bin/cluster.cgi?seq=CS0AQ004ZH10_A0368_l&cluster=10650.f.
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0AQ004ZH10_A0368_l:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50-NORMALIZED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAGACCATGTGCACCCTCATCACGGCCATGCATGCCAATAGTCAGTTCACCAGCACCTA 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="NEUROBLASTOMA COT 50-NORMALIZED" /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED /note="Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Scor wites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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BX367456.1 GI:30447638
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Pred. No. 1e-15;
0; Mismatches 184; Indels 0;
                   Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
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Contact: Genoscope

Contact: Genoscope

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BP 191 91006 EVRX cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 10650.f

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bhr/cluster.cgi?seq=CGOAQ004ZF10 A0366 1&cluster=10650.f.

Contact: Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ Invitroden Corporation 1600

Faraday Avenue Genoscope sequence ID : CSOAQ004ZF10_A0366_1.
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